



SEQUENCE LISTING

<110> Genentech, Inc. Ashkenazi, Avi Botstein, David Desnoyers, Luc Eaton, Dan L. Ferrara, Napoleone Filvaroff, Ellen Fong, Sherman Gao, Wei-Qiang Gerber, Hanspeter Gerritsen, Mary E. Goddard, A. Godowski, Paul J. Grimaldi, Christopher J. Gurney, Austin L. Hillan, Kenneth, J. Kljavin, Ivar J. Mather, Jennie P. Pan, James Paoni, Nicholas F. Roy, Margaret Ann Stewart, Timothy A. Tumas, Daniel Williams, P. Mickey Wood, William, I.

- <120> Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same
- <130> 10466-14
- <140> 09/665,350
- <141> 2000-09-18
- <150> PCT/US00/04414
- <151> 2000-02-22
- <150> US 60/143,048
- <151> 1999-07-07
- <150> US 60/145,698
- <151> 1999-07-26
- <150> US 60/146,222
- <151> 1999-07-28
- <150> PCT/US99/20594
- <151> 1999-09-08
- <150> PCT/US99/20944
- <151> 1999-09-13

```
<150> PCT/US99/21090
<151> 1999-09-15
<150> PCT/US99/21547
<151> 1999-09-15
<150> PCT/US99/23089
<151> 1999-10-05
<150> PCT/US99/28214
<151> 1999-11-29
<150> PCT/US99/28313
<151> 1999-11-30
<150> PCT/US99/28564
<151> 1999-12-02
<150> PCT/US99/28565
<151> 1999-12-02
<150> PCT/US99/30095
<151> 1999-12-16
<150> PCT/US99/30911
<151> 1999-12-20
<150> PCT/US99/30999
<151> 1999-12-20
<150> PCT/US00/00219
<151> 2000-01-05
<160> 423
<210> 1
<211> 1825
<212> DNA
<213> Homo sapiens
<400> 1
actgcacctc ggttctatcg attgaattcc ccggggatcc tctagagatc cctcgacctc 60
gacccaegeg teegggeegg ageageaegg cegeaggace tggageteeg getgegtett 120
cccgcagcgc tacccgccat gcgcctgccg cgccgggccg cgctggggct cctgccgctt 180
ctgctgctgc tgccgcccgc gccggaggcc gccaagaagc cgacgccctg ccaccggtgc 240
cgggggctgg tggacaagtt taaccagggg atggtggaca ccgcaaagaa gaactttggc 300
ggcgggaaca cggcttggga ggaaaagacg ctgtccaagt acgagtccag cgagattcgc 360
ctgctggaga tcctggaggg gctgtgcgag agcagcgact tcgaatgcaa tcagatgcta 420
gaggcgcagg aggagcacct ggaggcctgg tggctgcagc tgaagagcga atatcctgac 480
ttattcgagt ggttttgtgt gaagacactg aaagtgtgct gctctccagg aacctacggt 540
cccgactgtc tcgcatgcca gggcggatcc cagaggccct gcagcgggaa tggccactgc 600
```

ageggagatg ggageagaca gggegaeggg teetgeeggt geeacatggg gtaceaggge 660

```
cegetgtgea etgaetgeat ggaeggetae tteagetege teeggaaega gaeceaeage 720
atetgeacag eetgtgaega gteetgeaag aegtgetegg geetgaecaa cagagaetge 780
ggcgagtgtg aagtgggctg ggtgctggac gagggcgcct gtgtggatgt ggacgagtgt 840
geggeegage egecteeetg eagegetgeg eagttetgta agaacgeeaa eggeteetae 900
acqtqcqaaq aqtqtqactc caqctqtqtq qqctqcacaq qqqaaqqccc aqqaaactqt 960
aaagagtgta tetetggeta egegagggag caeggaeagt gtgeagatgt ggaegagtge 1020
tcactagcag aaaaaacctg tgtgaggaaa aacgaaaact gctacaatac tccagggagc 1080
tacgtetgtg tgtgteetga eggettegaa gaaaeggaag atgeetgtgt geegeeggea 1140
gaggetgaag ceacagaagg agaaageeeg acacagetge eeteeegega agacetgtaa 1200
tgtgccggac ttacccttta aattattcag aaggatgtcc cgtggaaaat gtggccctga 1260
ggatgccgtc tcctgcagtg gacagcggcg gggagaggct gcctgctctc taacggttga 1320
ttctcatttg tcccttaaac agctgcattt cttggttgtt cttaaacaga cttgtatatt 1380
aaaaaaaaaa aaagggcggc cgcgactcta gagtcgacct gcagaagctt ggccgccatg 1500
gcccaacttg tttattgcag cttataatgg ttacaaataa agcaatagca tcacaaattt 1560
cacaaataaa gcatttttt cactgcattc tagttgtggt ttgtccaaac tcatcaatgt 1620
atcttatcat gtctggatcg ggaattaatt cggcgcagca ccatggcctg aaataacctc 1680
tgaaagagga acttggttag gtaccttctg aggcggaaag aaccagctgt ggaatgtgtg 1740
tcagttaggg tgtggaaagt ccccaggctc cccagcaggc agaagtatgc aagcatgcat 1800
ctcaattagt cagcaaccca gtttt
<210> 2
<211> 353
<212> PRT
<213> Homo sapiens
<400> 2
Met Arg Leu Pro Arg Arg Ala Ala Leu Gly Leu Leu Pro Leu Leu
Leu Leu Pro Pro Ala Pro Glu Ala Ala Lys Lys Pro Thr Pro Cys His
Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr
Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
65
                                                           80
                    70
Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
                               105
Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys
       115
Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser
```

135

1825

Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg 145 150 Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu 165 170 Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr 185 His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp 210 215 Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro 225 230 Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys 245 250 Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly 260 Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys 290 295 300 Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro 305 310 Asp Gly Phe Glu Glu Thr Glu Asp Ala Cys Val Pro Pro Ala Glu Ala Glu Ala Thr Glu Gly Glu Ser Pro Thr Gln Leu Pro Ser Arg Glu Asp 340

Leu

<210> 3

<211> 2206

<212> DNA

<213> Homo sapiens

<400> 3

caggiccaac tgcaccicgg tictatcgat tgaaticccc ggggatcctc tagagatccc 60 tegaccicga cecaegegic egecaggeeg ggaggegaeg egecaageeg tetaaaeggg 120 aacageectg getgagggag etgeagegea geagagtate tgaeggegee aggitgegta 180 ggtgeggeae gaggagtitt eeeggeageg aggaggicet gageageatg geeeggagga 240

```
gegeetteee tgeegeegeg etetggetet ggageateet eetgtgeetg etggeaetge 300
gggcggaggc cgggccgccg caggaggaga gcctgtacct atggatcgat gctcaccagg 360
caagagtact cataggattt gaagaagata teetgattgt tteagagggg aaaatggeac 420
cttttacaca tqatttcaqa aaaqcqcaac aqaqaatqcc aqctattcct qtcaatatcc 480
attecatgaa ttttacetgg caagetgeag ggeaggeaga ataettetat gaatteetgt 540
cettgegete cetggataaa ggcatcatgg cagatecaac egteaatgte cetetgetgg 600
gaacagtgcc tcacaaggca tcagttgttc aagttggttt cccatgtctt ggaaaacagg 660
atggggtggc agcatttgaa gtggatgtga ttgttatgaa ttctgaaggc aacaccattc 720
tccaaacacc tcaaaatgct atcttcttta aaacatgtca acaagctgag tgcccaggcg 780
ggtgccgaaa tggaggcttt tgtaatgaaa gacgcatctg cgagtgtcct gatgggttcc 840
acqqacctca ctqtqaqaaa qccctttqta ccccacqatq tatqaatqqt ggactttqtq 900
tgactcctgg tttctgcatc tgcccacctg gattctatgg agtgaactgt gacaaagcaa 960
actgctcaac cacctgcttt aatggaggga cctgtttcta ccctggaaaa tgtatttgcc 1020
ctccaggact agagggagag cagtgtgaaa tcagcaaatg cccacaaccc tgtcgaaatg 1080
gaggtaaatg cattggtaaa agcaaatgta agtgttccaa aggttaccag ggagacctct 1140
gttcaaagcc tgtctgcgag cctggctgtg gtgcacatgg aacctgccat gaacccaaca 1200
aatgccaatg tcaagaaggt tggcatggaa gacactgcaa taaaaggtac gaagccagcc 1260
tcatacatgc cctgaggcca gcaggcgccc agctcaggca gcacacgcct tcacttaaaa 1320
aggccgagga gcggcgggat ccacctgaat ccaattacat ctggtgaact ccgacatctg 1380
aaacgtttta agttacacca agttcatagc ctttgttaac ctttcatgtg ttgaatgttc 1440
aaataatgtt cattacactt aagaatactg gcctgaattt tattagcttc attataaatc 1500
actgagetga tatttactet teettttaag ttttetaagt acgtetgtag catgatggta 1560
tagattttct tgtttcagtg ctttgggaca gattttatat tatgtcaatt gatcaggtta 1620
aaattttcag tgtgtagttg gcagatattt tcaaaattac aatgcattta tggtgtctgg 1680
gggcagggga acatcagaaa ggttaaattg ggcaaaaatg cgtaagtcac aagaatttgg 1740
atggtgcagt taatgttgaa gttacagcat ttcagatttt attgtcagat atttagatgt 1800
ttaccattat tccagagatt cagtattaaa aaaaaaaaa ttacactgtg gtagtggcat 1920
ttaaacaata taatatatto taaacacaat gaaataggga atataatgta tgaacttttt 1980
aaaaaaaaa aaaaaaaaa aaaaaaaaaa gggcggccgc gactctagag tcgacctgca 2160
gaagettgge egecatggee caacttgttt attgeagett ataatg
                                                            2206
<210> 4
<211> 379
<212> PRT
<213> Homo sapiens
<400> 4
```

Met Ala Arg Arg Ser Ala Phe Pro Ala Ala Leu Trp Leu Trp Ser

Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro Pro Gln 20 25

Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala 55

Pro Phe Thr His Asp Phe Arq Lys Ala Gln Gln Arq Met Pro Ala Ile

65					70					75					80
Pro	Val	Asn	Ile	His 85	Ser	Met	Asn	Phe	Thr 90	Trp	Gln	Ala	Ala	Gly 95	Gln
Ala	Glu	Tyr	Phe 100	Tyr	Glu	Phe	Leu	Ser 105	Leu	Arg	Ser	Leu	Asp 110	Lys	Gly
Ile	Met	Ala 115	Asp	Pro	Thr	Val	Asn 120	Val	Pro	Leu	Leu	Gly 125	Thr	Val	Pro
His	Lys 130	Ala	Ser	Val	Val	Gln 135	Val	Gly	Phe	Pro	Cys 140	Leu	Gly	Lys	Gln
Asp 145	Gly	Val	Ala	Ala	Phe 150	Glu	Val	Asp	Val	Ile 155	Val	Met	Asn	Ser	Glu 160
Gly	Asn	Thr	Ile	Leu 165	Gln	Thr	Pro	Gln	Asn 170	Ala	Ile	Phe	Phe	Lys 175	Thr
Cys	Gln	Gln	Ala 180	Glu	Cys	Pro	Gly	Gly 185	Cys	Arg	Asn	Gly	Gly 190	Phe	Cys
Asn	Glu	Arg 195	Arg	Ile	Cys	Glu	Cys 200	Pro	Asp	Gly	Phe	His 205	Gly	Pro	His
Cys	Glu 210	Lys	Ala	Leu	Cys	Thr 215	Pro	Arg	Cys	Met	Asn 220	Gly	Gly	Leu	Cys
Val 225	Thr	Pro	Gly	Phe	Cys 230	Ile	Cys-	Pro	Pro	Gly 235	Phe	Tyr	Gly	Val	Asn 240
Cys	Asp	Lys	Ala	Asn 245	Cys	Ser	Thr	Thr	Cys 250	Phe	Asn	Gly	Gly	Thr 255	Cys
Phe	Tyr	Pro	Gly 260	Lys	Cys	Ile	Cys	Pro 265	Pro	Gly	Leu	Glu	Gly 270	Glu	Gln
Cys	Glu	Ile 275	Ser	Lys	Cys	Pro	Gln 280		Cys	Arg	Asn	Gly 285	Gly	Lys	Cys
Ile	Gly 290	Lys	Ser	Lys	Cys	Lys 295	Cys	Ser	Lys	Gly	Tyr 300	Gln	Gly	Asp	Leu
Cys 305	Ser	Lys	Pro	Val	Cys 310	Glu	Pro	Gly	Cys	Gly 315	Ala	His	Gly	Thr	Cys 320
His	Glu	Pro	Asn	Lys 325	Cys	Gln	Cys	Gln	Glu 330	Gly	Trp	His	Gly	Arg 335	His
Cys	Asn	Lys	Arg 340	Tyr	Glu	Ala	Ser	Leu 345	Ile	His	Ala	Leu	Arg 350	Pro	Ala

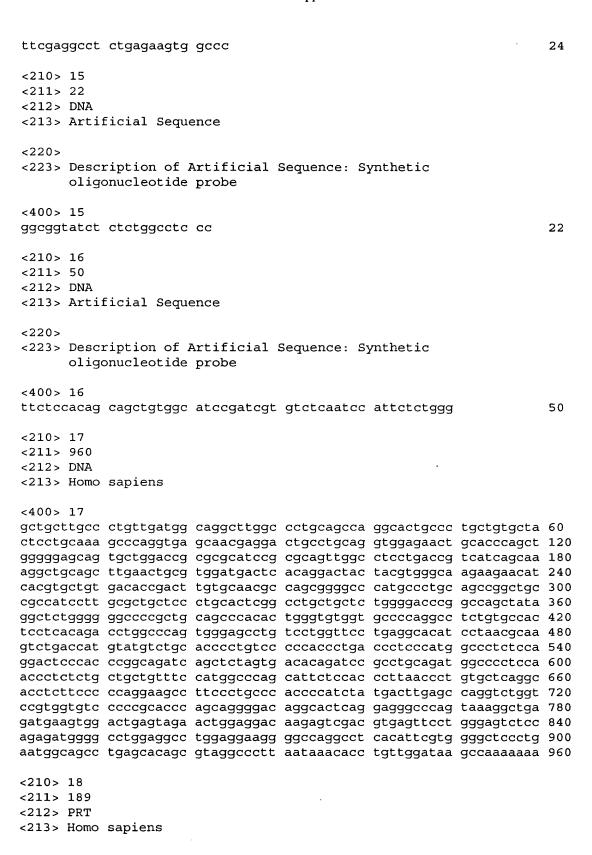
Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Lys Ala Glu Glu 355 360 365	
Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp 370 375	
<210> 5 <211> 45 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 5 agggagcacg gacagtgtgc agatgtggac gagtgctcac tagca	45
<210> 6 <211> 21 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 6 agagtgtatc tctggctacg c	21
<210> 7 <211> 22 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 7 taagtccggc acattacagg tc	22
<210> 8 <211> 49 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 8 cccacqatqt atqaatqqtq qactttqtqt qactcctqqt ttctqcatc	49

```
<210> 9
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
     oligonucleotide probe
<400> 9
aaagacgcat ctgcgagtgt cc
                                                                22
<210> 10
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
     oligonucleotide probe
<400> 10
tgctgatttc acactgctct ccc
                                                                23
<210> 11
<211> 2197
<212> DNA
<213> Homo sapiens
<400> 11
eggaegegtg ggegteegge ggtegeagag ceaggaggeg gaggegegeg ggeeageetg 60
ggccccagcc cacaccttca ccagggccca ggagccacca tgtggcgatg tccactgggg 120
ctactgctgt tgctgccgct ggctggccac ttggctctgg gtgcccagca gggtcgtggg 180
cgccgggagc tagcaccggg tctgcacctg cggggcatcc gggacgcggg aggccggtac 240
tgccaggage aggaectgtg etgeegegge egtgeegaeg aetgtgeeet geeetaeetg 300
ggcgccatct gttactgtga cctcttctgc aaccgcacgg tctccgactg ctgccctgac 360
ttetgggaet tetgeetegg egtgeeacee cetttteece egateeaagg atgtatgeat 420
ggaggtcgta tctatccagt cttgggaacg tactgggaca actgtaaccg ttgcacctgc 480
caggagaaca ggcagtggca tggtggatcc agacatgatc aaagccatca accagggcaa 540
ctatggctgg caggctggga accacagcgc cttctggggc atgaccctgg atgagggcat 600
tegetacege etgggeacea teegeecate tteeteggte atgaacatge atgaaattta 660
tacagtgctg aacccagggg aggtgcttcc cacagccttc gaggcctctg agaagtggcc 720
caacctgatt catgagcctc ttgaccaagg caactgtgca ggctcctggg ccttctccac 780
agcagetgtg geateegate gtgteteaat ceattetetg ggacacatga egeetgteet 840
gtcgccccag aacctgctgt cttgtgacac ccaccagcag cagggctgcc gcggtgggcg 900
tetegatggt geetggtggt teetgegteg eegaggggtg gtgtetgaee aetgetaeee 960
etteteggge egtgaaegag aegaggetgg ceetgegeee eeetgtatga tgeaeageeg 1020
agccatgggt cggggcaagc gccaggccac tgcccactgc cccaacagct atgttaataa 1080
caatgacate taccaggtea eteetgteta eegeetegge tecaaegaca aggagateat 1140
gaaggagctg atggagaatg gccctgtcca agccctcatg gaggtgcatg aggacttctt 1200
cctatacaag ggaggcatct acagccacac gccagtgagc cttgggaggc cagagagata 1260
```

His Asp Pro Gly

```
tggaaggacg ctcaaatact ggactgcggc caactcctgg ggcccagcct ggggcgagag 1380
gggccacttc cgcatcgtgc gcggcgtcaa tgagtqcqac atcqaqaqct tcqtqctqqq 1440
cgtctggggc cgcgtgggca tggaggacat ggqtcatcac tgaggctqcq qqcaccacqc 1500
ggggtccggc ctgggatcca ggctaagggc cggcggaaga ggccccaatg gggcggtgac 1560
cccagcetcg cccgacagag cccggggggc aggcgggcgc cagggcgcta atcccqqcqc 1620
gggttccgct gacgcagcgc cccgcctggg agccgcgggc aggcgagact qqcqqaqccc 1680
ccagacetee cagtggggae ggggeaggge etggeetggg aagageaeag etgeagatee 1740
caggoetetg gegeeceae teaagaetae caaageeagg acaceteaag tetecageee 1800
caatacccca ccccaatccc gtattctttt ttttttttt ttagacaggg tcttgctccg 1860
ttgcccaggt tggagtgcag tggcccatca qqqctcactq taacctccqa ctcctqqqtt 1920
caagtgaccc teceacetea geeteteaag tagetgggae taeaggtgea eeaceacace 1980
tggctaattt ttgtattttt tgtaaagagg ggggtctcac tgtgttgccc aggctggttt 2040
cgaactectg ggctcaagcg gtccacctgc ctccgcctcc caaagtgctg ggattgcagg 2100
catgagecae tgeacecage cetgtattet tattetteag atatttattt ttetttteae 2160
tgttttaaaa taaaaccaaa gtattgataa aaaaaaa
<210> 12
<211> 164
<212> PRT
<213> Homo sapiens
<400> 12
Met Trp Arg Cys Pro Leu Gly Leu Leu Leu Leu Pro Leu Ala Gly
His Leu Ala Leu Gly Ala Gln Gln Gly Arg Gly Arg Glu Leu Ala
Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys
         35
Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu
Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr
Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro
Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr
Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln
        115
                            120
                                                125
Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln
    130
Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly
                    150
                                        155
                                                            160
```

```
<210> 13
<211> 533
<212> DNA
<213> Homo sapiens
<220>
<221> modified base
<222> (33)
<223> a, t, c or g
<220>
<221> modified_base
<222> (80)
<223> a, t, c or g
<220>
<221> modified base
<222> (94)
<223> a, t, c or g
<220>
<221> modified base
<222> (144)
<223> a, t, c or g
<220>
<221> modified base
<222> (188)
<223> a, t, c or g
<400> 13
aggeteettg geeettttte cacageaage ttntgenate eegattegtt gteteaaate 60
caattetett gggacacatn acgcetgtee tttngceeca gaacetgetg tettgtacae 120
ccaccagcag cagggctgcc gcgntgggcg tctcgatggt gcctggtggt tcctgcgtcg 180
ccgagggntg gtgtctgacc actgctaccc cttctcgggc cgtgaacgag acgaggctgg 240
ccctgcgccc ccctgtatga tgcacagccg agccatgggt cggggcaagc gccaggccac 300
tgcccactgc cccaacagct atgttaataa caatgacatc taccaggtca ctcctgtcta 360
ccgcctcggc tccaacgaca aggagatcat gaaggagctg atggagaatg gccctgtcca 420
agccctcatg gaggtgcatg aggacttctt cctatacaag ggaggcatct acagccacac 480
gccagtgagc cttgggaggc cagagagata ccgccggcat gggacccact cag
<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 14
```



<400> 18 Met Thr His Arg Thr Thr Trp Ala Arg Arg Thr Ser Arg Ala Val Thr Pro Thr Cys Ala Thr Pro Ala Gly Pro Met Pro Cys Ser Arg Leu Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly 50 55 Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met 90 Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser 100 105 Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe 130 135 Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe 145 150 Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser 170 Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln 180 <210> 19 <211> 24 <212> DNA <213> Artificial Sequence

<220×

<400> 19 tgctgtgcta ctcctgcaaa gccc

<210> 20

<211> 24

<212> DNA

```
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 20
tgcacaagtc ggtgtcacag cacg
                                                                   24
<210> 21
<211> 44
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 21
agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg
                                                                   44
<210> 22
<211> 1200
<212> DNA
<213> Homo sapiens
<400> 22
cccacgcgtc cgaacctctc cagcgatggg agccgcccgc ctgctgccca acctcactct 60
gtgcttacag ctgctgattc tctgctgtca aactcagtac gtgagggacc agggcgccat 120
gaccgaccag ctgagcaggc ggcagatccg cgagtaccaa ctctacagca ggaccagtgg 180
caagcacgtg caggtcaccg ggcgtcgcat ctccgccacc gccgaggacg gcaacaagtt 240
tgccaagctc atagtggaga cggacacgtt tggcagccgg gttcgcatca aaggggctga 300
gagtgagaag tacatctqta tqaacaaqaq qqqcaaqctc atcqqqaaqc ccaqcqqqaa 360
gagcaaagac tgcgtgttca cggagatcgt gctggagaac aactatacgg ccttccagaa 420
cgcccggcac gagggctggt tcatggcctt cacgcggcag gggcggcccc gccaggcttc 480
cegeageege cagaaceage gegaggeeca etteateaag egeetetaee aaggeeaget 540
gcccttcccc aaccacgccg agaagcagaa gcagttcgag tttgtgggct ccgccccac 600
ccgccggacc aagcgcacac ggcggcccca gcccctcacg tagtctggga ggcagggggc 660
agcagecect gggeegecte eccaecectt teeettetta atecaaggae tgggetgggg 720
tggcgggagg ggagccagat ccccgaggga ggaccctgag ggccgcgaag catccgagcc 780
cccagctggg aaggggcagg ccggtgcccc aggggcggct ggcacagtgc ccccttcccg 840
gacgggtggc aggccctgga gaggaactga gtqtcaccct gatctcaggc caccagcctc 900
tgccggcctc ccaqccgqqc tcctqaaqcc cqctqaaaqq tcaqcqactq aaqqccttqc 960
agacaaccgt ctggaggtgg ctgtcctcaa aatctgcttc tcggatctcc ctcagtctgc 1020
ccccagcccc caaactcctc ctggctagac tgtaggaagg gacttttgtt tgtttgtttg 1080
tttcaggaaa aaagaaaggg agagagagga aaatagaggg ttgtccactc ctcacattcc 1140
acgacccagg cctgcacccc acccccaact cccagccccg gaataaaacc attttcctgc 1200
<210> 23
<211> 205
<212> PRT
<213> Homo sapiens
```

<400> 23

Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln Leu 1 5 10 15

Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met
20 25 30

Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser 35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala
50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp 65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr 85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys
100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr 115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg 130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu 145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn 165 170 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr 180 185 190

Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr
195 200 205

<210> 24

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<400> 24

cagtacgtga gggaccaggg cgccatga

28

```
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 25
ccggtgacct gcacgtgctt gcca
                                                                   24
<210> 26
<211> 41
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<220>
<221> modified base
<222> (21)
<223> a, t, c or g
<400> 26
geggatetge egeetgetea netggteggt catggegeee t
                                                                   41
<210> 27
<211> 2479
<212> DNA
<213> Homo sapiens
<400> 27
acttgccatc acctgttgcc agtgtggaaa aattctccct gttgaatttt ttgcacatgg 60
aggacagcag caaagaggc aacacaggct gataagacca gagacagcag ggagattatt 120
ttaccatacg ccctcaggac gttccctcta gctggagttc tggacttcaa cagaacccca 180
tocagteatt ttgattttgc tgtttatttt ttttttcttt ttctttttcc caccacattg 240
tattttattt ccgtacttca gaaatgggcc tacagaccac aaagtggccc agccatgggg 300
cttttttcct gaagtcttgg cttatcattt ccctggggct ctactcacag gtgtccaaac 360
tcctggcctg ccctagtgtg tgccgctgcg acaggaactt tgtctactgt aatgagcgaa 420
gettgaeete agtgeetett gggateeegg agggegtaae egtaetetae etecaeaaea 480
accaaattaa taatgctgga tttcctgcag aactgcacaa tgtacagtcg gtgcacacgg 540
tctacctgta tggcaaccaa ctggacgaat tccccatgaa ccttcccaag aatgtcagag 600
ttctccattt gcaggaaaac aatattcaga ccatttcacg ggctgctctt gcccagctct 660
tgaagettga agagetgeac etggatgaca actecatate cacagtgggg gtggaaqaeq 720
gggccttccg ggaggctatt agcctcaaat tgttgttttt gtctaagaat cacctgagca 780
gtgtgcctgt tgggcttcct gtggacttgc aagagctgaq agtgqatgaa aatcgaattg 840
ctgtcatatc cqacatgqcc ttccaqaatc tcacqaqctt qqaqcqtctt attgtqqacq 900
ggaacctcct gaccaacaag ggtatcgccg agggcacctt cagccatctc accaagctca 960
aggaattttc aattgtacgt aattcgctgt cccaccctcc tcccgatctc ccaggtacgc 1020
atotgatcag gototatttg caggacaacc agataaacca cattcotttg acagcottot 1080
caaatctgcg taagctggaa cggctggata tatccaacaa ccaactgcgg atgctgactc 1140
```

```
aaggggtttt tgataatete teeaacetga ageageteae tgeteggaat aaceettggt 1200
tttgtgactg cagtattaaa tgggtcacag aatggctcaa atatatccct tcatctctca 1260
acgtgcgggg tttcatqtqc caaqqtcctq aacaaqtccq gqqqatqqcc qtcaqqqaat 1320
taaatatqaa tottttqtcc tqtcccacca cqacccccqq cctqcctctc ttcaccccaq 1380
ccccaagtac agcttctccg accactcagc ctcccaccct ctctattcca aaccctagca 1440
gaagetacae geeteeaact ectaecaeat egaaacttee caegatteet gaetgggatg 1500
gcagagaaag agtgacccca cctatttctg aacggatcca gctctctatc cattttgtga 1560
atgatacttc cattcaagtc agctggctct ctctcttcac cgtgatggca tacaaactca 1620
catgggtgaa aatgggccac agtttagtag ggggcatcgt tcaggagcgc atagtcagcg 1680
gtgagaagca acacctgagc ctggttaact tagagccccg atccacctat cggatttgtt 1740
tagtgccact ggatgctttt aactaccgcg cggtagaaga caccatttgt tcagaggcca 1800
ccacccatgc ctcctatctg aacaacggca gcaacacagc gtccagccat gagcagacga 1860
cgtcccacag catgggctcc ccctttctgc tggcgggctt gatcgggggc gcggtgatat 1920
ttgtgctggt ggtcttgctc agcgtctttt gctggcatat gcacaaaaag gggcgctaca 1980
cctcccagaa gtggaaatac aaccggggcc ggcggaaaga tgattattgc gaggcaggca 2040
ccaagaagga caactccatc ctggagatga cagaaaccag ttttcagatc gtctccttaa 2100
ataacgatca actoottaaa ggagatttoa gactgoagoo catttacaco ccaaatgggg 2160
gcattaatta cacagactgc catatcccca acaacatgcg atactgcaac agcagcgtgc 2220
cagacetgga geactgeeat acgtgacage cagaggeeca gegttateaa ggeggacaat 2280
tagactettg agaacacact egtgtgtgca cataaagaca egcagattae atttgataaa 2340
tgttacacag atgcatttgt gcatttgaat actctgtaat ttatacggtg tactatataa 2400
tgggatttaa aaaaagtgct atcttttcta tttcaagtta attacaaaca gttttgtaac 2460
tctttgcttt ttaaatctt
<210> 28
<211> 660
<212> PRT
<213> Homo sapiens
<400> 28
Met Gly Leu Gln Thr Thr Lys Trp Pro Ser His Gly Ala Phe Phe Leu
                  5
                                     10
Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys
             20
                                 25
Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr
Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
     50
Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe
 65
Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
                 85
                                     90
Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
            100
                                105
                                                    110
Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala
```

120

125

- Leu Ala Gln Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser
 130 135 140
- Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser 145 150 155 160
- Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val
 165 170 175
- Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile 180 185 190
- Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg 195 200 205
- Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly 210 220
- Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn 225 230 235 240
- Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg
 245 250 255
- Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe
 260 265 270
- Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu 275 280 285
- Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln 290 295 300
- Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp 305 310 315 320
- Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly 325 330 335
- Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu
 340 345 350
- Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Thr Pro Gly Leu Pro 355 360 365
- Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro 370 375 380
- Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro 385 390 395 400
- Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

				405					410					415	
Val	Thr	Pro	Pro 420	Ile	Ser	Glu	Arg	Ile 425	Gln	Leu	Ser	Ile	His 430	Phe	Val
Asn	Asp	Thr 435	Ser	Ile	Gln	Val	Ser 440	Trp	Leu	Ser	Leu	Phe 445	Thr	Val	Met
Ala	Tyr 450	Lys	Leu	Thr	Trp	Val 455	Lys	Met	Gly	His	Ser 460	Leu	Val	Gly	Gly
Ile 465	Val	Gln	Glu	Arg	Ile 470	Val	Ser	Gly	Glu	Lys 475	Gln	His	Leu	Ser	Leu 480
Val	Asn	Leu	Glu	Pro 485	Arg	Ser	Thr	Tyr	Arg 490	Ile	Cys	Leu	Val	Pro 495	Leu
Asp	Ala	Phe	Asn 500	Tyr	Arg	Ala	Val	Glu 505	Asp	Thr	Ile	Cys	Ser 510	Glu	Ala
Thr	Thr	His 515	Ala	Ser	Tyr	Leu	Asn 520	Asn	Gly	Ser	Asn	Thr 525	Ala	Ser	Ser
His	Glu 530	Gln	Thr	Thr	Ser	His 535	Ser	Met	Gly	Ser	Pro 540	Phe	Leu	Leu	Ala
Gly 545	Leu	Ile	Gly	Gly	Ala 550	Val	Ile	Phe	Val	Leu 555	Val	Val	Leu	Leu	Ser 560
Val	Phe	Cys	Trp	His 565	Met	His	Lys	Lys	Gly 570	Arg	Tyr	Thr	Ser	Gln 575	Lys
Trp	Lys	Tyr	Asn 580	Arg	Gly	Arg	Arg	Lys 585	Asp	Asp	Tyr	Cys	Glu 590	Ala	Gly
Thr	Lys	Lys 595	Asp	Asn	Ser	Ile	Leu 600	Glu	Met	Thr	Glu	Thr 605	Ser	Phe	Gln
Ile	Val 610	Ser	Leu	Asn	Asn	Asp 615	Gln	Leu	Leu	Lys	Gly 620	Asp	Phe	Arg	Leu
Gln 625	Pro	Ile	Tyr	Thr	Pro 630	Asn	Gly	Gly	Ile	Asn 635	Tyr	Thr	Asp	Cys	His 640
Ile	Pro	Asn	Asn	Met 645	Arg	Tyr	Cys	Asn	Ser 650	Ser	Val	Pro	Asp	Leu 655	Glu
His	Cys	His	Thr 660												
<210)> 29)													
<211	.> 21	_													
<212	2 > DN	ΙA													

<213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 29 cggtctacct gtatggcaac c	21
<210> 30 <211> 22 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 30 gcaggacaac cagataaacc ac	22
<210> 31 <211> 22 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 31 acgcagattt gagaaggctg tc	22
<210> 32 <211> 46 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 32 ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac	46
<210> 33 <211> 3449 <212> DNA <213> Homo sapiens	
<400> 33 acttggagca ageggeggeg geggagacag aggeagagge agaagetggg geteegteet egeeteeac gagegateec egaggagag egeggeete ggegaggega agaggegae	

gaggaagacc cgggtggctg cgcccttgcc tcgcttccca ggcgccggcg gctgcagcct 180 tgcccctctt gctcgccttg aaaatggaaa agatgctcgc aggctgcttt ctgctgatcc 240 teggacagat egteeteete eetgeegagg eeagggageg gteaegtggg aggteeatet 300 ctaggggcag acacgctcgg acccacccgc agacggccct tctggagagt tcctgtgaga 360 acaagcgggc agacctggtt ttcatcattg acagctctcg cagtgtcaac acccatgact 420 atgcaaaggt caaggagttc atcgtggaca tcttgcaatt cttggacatt ggtcctgatg 480 tcacccgagt gggcctgctc caatatggca gcactgtcaa gaatgagttc tccctcaaga 540 ccttcaagag gaagtccgag gtggagcgtg ctgtcaagag gatgcggcat ctgtccacgg 600 gcaccatgac tgggctggcc atccagtatg ccctgaacat cgcattctca gaagcagagg 660 gggcccggcc cctgagggag aatgtgccac gggtcataat gatcgtgaca gatgggagac 720 ctcaggactc cgtggccgag gtggctgcta aggcacggga cacgggcatc ctaatctttg 780 ccattggtgt gggccaggta gacttcaaca ccttgaagtc cattgggagt gagccccatg 840 aggaccatgt cttccttgtg gccaatttca gccagattga gacgctgacc tccgtgttcc 900 agaagaagtt gtgcacggcc cacatgtgca gcaccctgga gcataactgt gcccacttct 960 gcatcaacat ccctggctca tacgtctgca ggtgcaaaca aggctacatt ctcaactcgg 1020 atcagacgac ttgcagaatc caggatctgt gtgccatgga ggaccacaac tgtgagcagc 1080 tetgtgtgaa tgtgeeggge teettegtet geeagtgeta eagtggetae geeetggetg 1140 aggatgggaa gaggtgtgtg gctgtggact actgtgcctc agaaaaccac ggatgtgaac 1200 atgagtgtgt aaatgctgat ggctcctacc tttgccagtg ccatgaagga tttgctctta 1260 acccagatga aaaaacgtgc acaaggatca actactgtgc actgaacaaa ccgggctgtg 1320 agcatgagtg cgtcaacatg gaggagagct actactgccg ctgccaccgt ggctacactc 1380 tggaccccaa tggcaaaacc tgcagccgag tggaccactg tgcacagcag gaccatggct 1440 gtgagcagct gtgtctgaac acggaggatt ccttcgtctg ccagtgctca gaaggcttcc 1500 tcatcaacga ggacctcaag acctgctccc gggtggatta ctgcctgctg agtgaccatg 1560 gttgtgaata ctcctgtgtc aacatggaca gatcctttgc ctgtcagtgt cctgagggac 1620 acgtgctccg cagcgatggg aagacgtgtg caaaattgga ctcttgtgct ctgggggacc 1680 acggttgtga acattcgtgt gtaagcagtg aagattcgtt tgtgtgccag tgctttgaag 1740 gttatatact ccgtgaagat ggaaaaacct gcagaaggaa agatgtctgc caagctatag 1800 accatggctg tgaacacatt tgtgtgaaca gtgacgactc atacacgtgc gagtgcttgg 1860 agggattccg gctcgctgag gatgggaaac gctgccgaag gaaggatgtc tgcaaatcaa 1920 cccaccatgg ctgcgaacac atttgtgtta ataatgggaa ttcctacatc tgcaaatgct 1980 cagagggatt tgttctagct gaggacggaa gacggtgcaa gaaatgcact gaaggcccaa 2040 ttgacctggt ctttgtgatc gatggatcca agagtcttgg agaagagaat tttgaggtcg 2100 tgaagcagtt tgtcactgga attatagatt ccttgacaat ttcccccaaa gccgctcgag 2160 tggggctgct ccagtattcc acacaggtcc acacagagtt cactctgaga aacttcaact 2220 cagccaaaga catgaaaaaa gccgtggccc acatgaaata catgggaaag ggctctatga 2280 ctgggctggc cctgaaacac atgtttgaga gaagttttac ccaaggagaa ggggccaggc 2340 ccetttecae aagggtgeee agageageea ttgtgtteae egaeggaegg geteaggatg 2400 acgtctccga gtgggccagt aaagccaagg ccaatggtat cactatgtat gctgttgggg 2460 taggaaaagc cattgaggag gaactacaag agattgcctc tgagcccaca aacaagcatc 2520 tettetatge egaagaette ageacaatgg atgagataag tgaaaaaaete aagaaaggea 2580 tctgtgaagc tctagaagac tccgatggaa gacaggactc tccagcaggg gaactgccaa 2640 aaacggtcca acagccaaca gaatctgagc cagtcaccat aaatatccaa gacctacttt 2700 cctgttctaa ttttgcagtg caacacagat atctgtttga agaagacaat cttttacggt 2760 ctacacaaaa gctttcccat tcaacaaaac cttcaggaag ccctttggaa gaaaaacacg 2820 atcaatgcaa atgtgaaaac cttataatgt tccagaacct tgcaaacgaa gaagtaagaa 2880 aattaacaca gcgcttagaa gaaatgacac agagaatgga agccctggaa aatcgcctga 2940 gatacagatg aagattagaa atcgcgacac atttgtagtc attgtatcac ggattacaat 3000 gaacgcagtg cagagcccca aagctcaggc tattgttaaa tcaataatgt tgtgaagtaa 3060 aacaatcagt actgagaaac ctggtttgcc acagaacaaa gacaagaagt atacactaac 3120 ttgtataaat ttatctagga aaaaaatcct tcagaattct aagatgaatt taccaggtga 3180 gaatgaataa gctatgcaag gtattttgta atatactgtg gacacaactt gcttctgcct 3240 catcctgcct tagtgtgcaa tctcatttga ctatacgata aagtttgcac agtcttactt 3300

ctgtagaaca ctggccatag gaaatgctgt ttttttgtac tggactttac cttgatatat 3360 gtatatggat gtatgcataa aatcatagga catatgtact tgtggaacaa gttggatttt 3420 ttatacaata ttaaaattca ccacttcag 3449

<210> 34

<211> 915

<212> PRT

<213> Homo sapiens

<400> 34

Met Glu Lys Met Leu Ala Gly Cys Phe Leu Leu Ile Leu Gly Gln Ile 1 5 10 15

Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile
20 25 30

Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu 35 40 45

Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser 50 55 60

Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile 65 70 75 80

Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val
85 90 95

Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys 100 105 110

Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg 115 120 125

His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu 130 135 140

Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser 165 170 175

Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe 180 185 190

Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly
195 200 205

Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln 210 215 220

Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

225					230					235					240
Met	Cys	Ser	Thr	Leu 245	Glu	His	Asn	Cys	Ala 250	His	Phe	Cys	Ile	Asn 255	Il ϵ
Pro	Gly	Ser	Tyr 260	Val	Cys	Arg	Cys	Lys 265	Gln	Gly	Tyr	Ile	Leu 270	Asn	Ser
Asp	Gln	Thr 275	Thr	Cys	Arg	Ile	Gln 280	Asp	Leu	Cys	Ala	Met 285	Glu	Asp	His
Asn	Cys 290	Glu	Gln	Leu	Cys	Val 295	Asn	Val	Pro	Gly	Ser 300	Phe	Val	Cys	Gln
Cys 305	Tyr	Ser	Gly	Tyr	Ala 310	Leu	Ala	Glu	Asp	Gly 315	Lys	Arg	Cys	Val	Ala 320
Val	Asp	Tyr	Cys	Ala 325	Ser	Glu	Asn	His	Gly 330	Cys	Glu	His	Glu	Cys 335	Val
Asn	Ala	Asp	Gly 340	Ser	Tyr	Leu	Cys	Gln 345	Cys	His	Glu	Gly	Phe 350	Ala	Leu
Asn	Pro	Asp 355	Glu	Lys	Thr	Cys	Thr 360	Arg	Ile	Asn	Tyŗ	Cys 365	Ala	Leu	Asn
Lys	Pro 370	Gly	Cys	Glu	His	Glu 375	Cys	Val	Asn	Met	Glu 380	Glu	Ser	Tyr	Tyr
Cys 385	Arg	Cys	His	Arg	Gly 390	Tyr	Thr	Leu	Asp	Pro 395	Asn	Gly	Lys	Thr	Cys 400
Ser	Arg	Val	Asp	His 405	Cys	Ala	Gln	Gln	Asp 410	His	Gly	Cys	Glu	Gln 415	Leu
Cys	Leu	Asn	Thr 420	Glu	Asp	Ser	Phe	Val 425	Сув	Gln	Суѕ	Ser	Glu 430	Gly	Phe
Leu	Ile	Asn 435	Glu	Asp	Leu	Lys	Thr 440	Cys	Ser	Arg	Val	Asp 445	Tyr	Cys	Leu
Leu	Ser 450	Asp	His	Gly	Cys	Glu 455	Tyr	Ser	Cys	Val	Asn 460	Met	Asp	Arg	Ser
Phe 465	Ala	Cys	Gln	Cys	Pro 470	Glu	Gly	His	Val	Leu 475	Arg	Ser	Asp	Gly	Lys 480
Thr	Cys	Ala	Lys	Leu 485	Asp	Ser	Cys	Ala	Leu 490	Gly	Asp	His	Gly	Cys 495	Glu
His	Ser	Cys	Val 500	Ser	Ser	Glu	Asp	Ser 505	Phe	Val	Cys	Gln	Cys 510	Phe	Glu

- Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val 515 520 525
- Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp 530 535 540
- Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp 545 550 555 560
- Gly Lys Arg Cys Arg Lys Asp Val Cys Lys Ser Thr His His Gly 565 570 575
- Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys 580 585 590
- Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Cys 595 600 605
- Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser 610 620
- Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile 625 630 635 640
- Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu 645 650 655
- Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn 660 665 670
- Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly 675 680 685
- Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser 690 695 700
- Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg 705 710 715 720
- Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu
 725 730 735
- Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly
 740 745 750
- Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro 755 760 765
- Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu 770 780
- Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser 785 790 795 800

Asp G	ly	Arg	Gln	Asp 805	Ser	Pro	Ala	Gly	Glu 810	Leu	Pro	Lys	Thr	Val 815	Gln	
Gln P	ro	Thr	Glu 820	Ser	Glu	Pro	Val	Thr 825	Ile	Asn	Ile	Gln	Asp 830	Leu	Leu	
Ser C		Ser 835	Asn	Phe	Ala	Val	Gln 840	His	Arg	Tyr	Leu	Phe 845	Glu	Glu	Asp	
Asn Le	eu 50	Leu	Arg	Ser	Thr	Gln 855	Lys	Leu	Ser	His	Ser 860	Thr	Lys	Pro	Ser	
Gly Se 865	er	Pro	Leu	Glu	Glu 870	Lys	His	Asp	Gln	Cys 875	Lys	Cys	Glu	Asn	Leu 880	
Ile M	et	Phe	Gln	Asn 885	Leu	Ala	Asn	Glu	Glu 890	Val	Arg	Lys	Leu	Thr 895	Gln	
Arg L	eu	Glu	Glu 900	Met	Thr	Gln	Arg	Met 905	Glu	Ala	Leu	Glu	Asn 910	Arg	Leu	
Arg T	yr	Arg 915														
<210><211><212><212><213>	23 DN	IA	icia	l Sed	quenc	ce										
<220> <223>			_	on or eotic			cial	Seq	uence	e: Sy	ynthe	etic				
<400>			- -			~~										23
gtgac	CCL	.gg t	rtgt	gaat	ac to	JC										23
<210>																
<211><212>																
<213>			icia	l Sed	quen	ce										
<220> <223>				on o: eotid			cial	Seq	uenc	e: S	ynth	etic				
<400>	36	5														
acago			cta	tagc	tt g	3										22
<210>	27	,														
<210>																
<212>																

<213> Artificial Sequence

```
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 37
gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag
                                                                  45
<210> 38
<211> 1813
<212> DNA
<213> Homo sapiens
<400> 38
ggagccgccc tgggtgtcag cggctcggct cccgcgcacg ctccggccgt cgcgcagcct 60
cgqcacctgc aggtccgtqc gtcccgcggc tggcgcccct gactccgtcc cggccaggga 120
gggccatgat ttccctcccg gggcccctgg tgaccaactt gctgcggttt ttgttcctgg 180
gqctgagtgc cctcgcgccc ccctcgcggg cccagctgca actgcacttg cccgccaacc 240
ggttgcaggc ggtggaggga ggggaagtgg tgcttccagc gtggtacacc ttgcacgggg 300
aggtgtette ateccageea tgggaggtge cetttgtgat gtggttette aaacagaaag 360
aaaaggagga tcaggtgttg tcctacatca atggggtcac aacaagcaaa cctggagtat 420
ccttggtcta ctccatgccc tcccggaacc tgtccctgcg gctggagggt ctccaggaga 480
aagactctgg cccctacagc tgctccgtga atgtgcaaga caaacaaggc aaatctaggg 540
gccacagcat caaaacctta gaactcaatg tactggttcc tccagctcct ccatcctgcc 600
gtetecaggg tgtgececat gtgggggeaa aegtgaeeet gagetgeeag tetecaagga 660
gtaagcccgc tgtccaatac cagtgggatc ggcagcttcc atccttccag actttctttg 720
caccagcatt agatgtcatc cgtgggtctt taagectcac caacettteg tettecatgg 780
ctggagtcta tgtctgcaag gcccacaatg aggtgggcac tgcccaatgt aatgtgacgc 840
tggaagtgag cacagggcct ggagctgcag tggttgctgg agctgttgtg ggtaccctgg 900
ttggactggg gttgctggct gggctggtcc tcttgtacca ccgccggggc aaggccctgg 960
aggagecage caatgatate aaggaggatg ceattgetee eeggaceetg eeetggeeca 1020
agageteaga cacaatetee aagaatggga ceettteete tgteacetee geaegageee 1080
teeggecace ceatggeest eccaggeetg gtgcattgac ceccaegees agtetetesa 1140
gccaggccct gccctcacca agactgccca cgacagatgg ggcccaccct caaccaatat 1200
cccccatccc tggtggggtt tettectetg gettgageeg catgggtget gtgcctgtga 1260
tggtgcctgc ccagagtcaa gctggctctc tggtatgatg accccaccac tcattggcta 1320
aaggatttgg ggtctctcct tcctataagg gtcacctcta gcacagaggc ctgagtcatg 1380
ggaaagagte acacteetga eeettagtae tetgeeecca eetetetta etgtgggaaa 1440
accateteag taagaeetaa gtgteeagga gacagaagga gaagaggaag tggatetgga 1500
attgggagga gcctccaccc acccctgact cctccttatg aagccagctg ctgaaattag 1560
ctactcacca agagtgaggg gcagagactt ccagtcactg agtctcccag gcccccttga 1620
tetgtacece acceptatet aacaceacee ttggetecea etccagetee etgtattgat 1680
ataacctqtc aqqctqqctt gqttaqqttt tactqqqqca gaggataqgg aatctcttat 1740
taaaactaac atqaaatatg tqttqttttc atttqcaaat ttaaataaaq atacataatg 1800
                                                                  1813
tttqtatqaa aaa
<210> 39
<211> 390
<212> PRT
<213> Homo sapiens
```

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

1				5					10					15	
Phe	Leu	Gly	Leu 20	Ser	Ala	Leu	Ala	Pro 25	Pro	Ser	Arg	Ala	Gln 30	Leu	Gln
Leu	His	Leu 35	Pro	Ala	Asn	Arg	Leu 40	Gln	Ala	Val	Glu	Gly 45	Gly	Glu	Val
Val	Leu 50	Pro	Ala	Trp	Tyr	Thr 55	Leu	His	Gly	Glu	Val 60	Ser	Ser	Ser	Gln
Pro 65	Trp	Glu	Val	Pro	Phe 70	Val	Met	Trp	Phe	Phe 75	Lys	Gln	Lys	Glu	Lys 80
Glu	Asp	Gln	Val	Leu 85	Ser	Tyr	Ile	Asn	Gly 90	Val	Thr	Thr	Ser	Lys 95	Pro
Gly	Val	Ser	Leu 100	Val	Tyr	Ser	Met	Pro 105	Ser	Arg	Asn	Leu	Ser 110	Leu	Arg
Leu	Glu	Gly 115	Leu	Gln	Glu	Lys	Asp 120	Ser	Gly	Pro	Tyr	Ser 125	Cys	Ser	Val
Asn	Val 130	Gln	Asp	Lys	Gln	Gly 135	Lys	Ser	Arg	Gly	His 140	Ser	Ile	Lys	Thr
Leu 145	Glu	Leu	Asn	Val	Leu 150	Val	Pro	Pro	Ala	Pro 155	Pro	Ser	Cys	Arg	Leu 160
Gln	Gly	Val	Pro	His 165	Val	Gly	Ala	Asn	Val 170	Thr	Leu	Ser	Cys	Gln 175	Ser
Pro	Arg	Ser	Lys 180	Pro	Ala	Val	Gln	Tyr 185	Gln	Trp	Asp	Arg	Gln 190	Leu	Pro
Ser	Phe	Gln 195	Thr	Phe	Phe	Ala	Pro 200	Ala	Leu	Asp	Val	Ile 205	Arg	Gly	Ser
Leu	Ser 210	Leu	Thr	Asn	Leu	Ser 215	Ser	Ser	Met	Ala	Gly 220	Val	Tyr	Val	Cys
Lys 225	Ala	His	Asn	Glu	Val 230	Gly	Thr	Ala	Gln	Cys 235	Asn	Val	Thr	Leu	Glu 240
Val	Ser	Thr	Gly	Pro 245	Gly	Ala	Ala	Val	Val 250	Ala	Gly	Ala	Val	Val 255	Gly
Thr	Leu	Val	Gly 260	Leu	Gly	Leu	Leu	Ala 265	Gly	Leu	Val	Leu	Leu 270	Tyr	His
Arg	Arg	Gly 275	Lys	Ala	Leu	Glu	Glu 280	Pro	Ala	Asn	Asp	Ile 285	Lys	Glu	Asp

Ala	Ile 290	Ala	Pro	Arg	Thr	Leu 295	Pro	Trp	Pro	Lys	Ser 300	Ser	Asp	Thr	Ile	
Ser 305	Lys	Asn	Gly	Thr	Leu 310	Ser	Ser	Val	Thr	Ser 315	Ala	Arg	Ala	Leu	Arg 320	
Pro	Pro	His	Gly	Pro 325	Pro	Arg	Pro	Gly	Ala 330	Leu	Thr	Pro	Thr	Pro 335	Ser	
Leu	Ser	Ser	Gln 340	Ala	Leu	Pro	Ser	Pro 345	Arg	Leu	Pro	Thr	Thr 350	Asp	Gly	
Ala	His	Pro 355	Gln	Pro	Ile	Ser	Pro 360	Ile	Pro	Gly	Gly	Val 365	Ser	Ser	Ser	
Gly	Leu 370	Ser	Arg	Met	Gly	Ala 375	Val	Pro	Val	Met	Val 380	Pro	Ala	Gln	Ser	
Gln 385	Ala	Gly	Ser	Leu	Val 390											
)> 40 L> 22															
<212	2> Di	1A		l Coa	~	7.0										
		CIL	icia.	l Sec	queno	ce										
<220 <223	3 > De		_	on of			cial	Seqi	ience	e: S	ynthe	etic			•	
<400)> 40)														
aggg	gtcto	cca g	ggaga	aaaga	ac to	2										22
)> 43 L> 24															
<212	2> Di	1A	i a i a '	l Sec	nien/	3.6										
			icia.	1 360	4uem											
<220 <223	3 > De			on of				Seq	ience	e: Sy	ynthe	etic				
)> 41 gtggg		tgca	agaca	at ag	gac										24
)> 42															
<212	L> 50 2> Di	1A														
<213	3 > A1	tif:	icia	l Sec	quen	ce										
<220			inti	on of	F 71 204	-161	aial	80~	1APC	<u>.</u>	ant h	atio				
\443			-	eotic			crar	seq.	TETTC6	. o	y 11 C 11	CLC				

<400> 42 ggccacagca tcaaaacctt agaactcaat gtactggttc ctccagctcc	50
<210> 43 <211> 18 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 43 gtgtgacaca gcgtgggc	18
<210> 44 <211> 18 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 44 gaccggcagg cttctgcg	18
<210> 45 <211> 25 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 45 cagcagette agecaceagg agtgg	25
<210> 46 <211> 24 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 46 ctgagccgtg ggctgcagtc tcgc	24
210 47	

```
<211> 45
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 47
                                                                  45
ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc
<210> 48
<211> 2822
<212> DNA
<213> Homo sapiens
<400> 48
eqceaecact geggeeaccg ecaatgaaac geeteeeget eetagtggtt tttteeactt 60
tgttgaattg ttcctatact caaaattgca ccaagacacc ttgtctccca aatgcaaaat 120
gtgaaatacg caatggaatt gaagcctgct attgcaacat gggattttca ggaaatggtg 180
tcacaatttg tgaagatgat aatgaatgtg gaaatttaac tcagtcctgt ggcgaaaatg 240
ctaattgcac taacacagaa ggaagttatt attgtatgtg tgtacctggc ttcagatcca 300
qcaqtaacca agacaggttt atcactaatg atggaaccgt ctgtatagaa aatgtgaatg 360
caaactgcca tttagataat gtctgtatag ctgcaaatat taataaaact ttaacaaaaa 420
tcagatccat aaaagaacct gtggctttgc tacaagaagt ctatagaaat tctgtgacag 480
atctttcacc aacagatata attacatata tagaaatatt agctgaatca tcttcattac 540
taggttacaa gaacaacact atctcagcca aggacaccct ttctaactca actcttactg 600
aatttgtaaa aaccgtgaat aattttgttc aaagggatac atttgtagtt tgggacaagt 660
tatctgtgaa tcataggaga acacatctta caaaactcat gcacactgtt gaacaagcta 720
ctttaaggat atcccagagc ttccaaaaga ccacagagtt tgatacaaat tcaacggata 780
tagctctcaa agttttcttt tttgattcat ataacatgaa acatattcat cctcatatga 840
atatggatgg agactacata aatatatttc caaagagaaa agctgcatat gattcaaatg 900
gcaatgttgc agttgcattt ttatattata agagtattgg tcctttgctt tcatcatctg 960
acaacttctt attgaaacct caaaattatg ataattctga agaggaggaa agagtcatat 1020
cttcagtaat ttcagtctca atgagctcaa acccacccac attatatgaa cttgaaaaaa 1080
taacatttac attaagtcat cgaaaggtca cagataggta taggagtcta tgtgcatttt 1140
ggaattactc acctgatacc atgaatggca gctggtcttc agagggctgt gagctgacat 1200
actcaaatga gacccacacc tcatgccgct gtaatcacct gacacatttt gcaattttga 1260
tqtcctctqq tccttccatt qqtattaaaq attataatat tcttacaagq atcactcaac 1320
taggaataat tatttcactq atttqtcttq ccatatqcat ttttaccttc tggttcttca 1380
gtgaaattca aagcaccagg acaacaattc acaaaaatct ttgctgtagc ctatttcttg 1440
ctgaacttgt ttttcttgtt gggatcaata caaatactaa taagctcttc tgttcaatca 1500
ttgccggact gctacactac ttctttttag ctgcttttgc atggatgtgc attgaaggca 1560
tacatctcta tctcattgtt gtgggtgtca tctacaacaa gggatttttg cacaagaatt 1620
tttatatett tggetateta ageceageeg tggtagttgg atttteggea geactaggat 1680
acagatatta tggcacaacc aaagtatgtt ggcttagcac cgaaaacaac tttatttgga 1740
gttttatagg accagcatgc ctaatcattc ttgttaatct cttggctttt ggagtcatca 1800
tatacaaaqt ttttcgtcac actgcagggt tgaaaccaga agttagttgc tttgagaaca 1860
taaggtettg tgcaagagga geeetegete ttetgtteet teteggeace acetggatet 1920
ttqqqqttct ccatqttqtq cacqcatcaq tqqttacagc ttacctcttc acagtcagca 1980
atgettteea ggggatgtte atttttttat teetgtgtgt tttatetaga aagatteaag 2040
aagaatatta cagattgttc aaaaatgtcc cctgttgttt tggatgttta aggtaaacat 2100
agagaatggt ggataattac aactgcacaa aaataaaaat tccaagctgt ggatgaccaa 2160
```

```
tgtataaaaa tgactcatca aattatccaa ttattaacta ctagacaaaa agtattttaa 2220
atcagttttt ctgtttatgc tataggaact gtagataata aggtaaaatt atgtatcata 2280
tagatatact atgtttttct atgtgaaata gttctgtcaa aaatagtatt gcagatattt 2340
ggaaagtaat tggtttctca ggagtgatat cactgcaccc aaggaaagat tttctttcta 2400
acacgagaag tatatgaatg teetgaagga aaccaetgge ttgatattte tgtgaetegt 2460
gttgcctttg aaactagtcc cctaccacct cggtaatgag ctccattaca gaaagtggaa 2520
cataagagaa tgaaggggca gaatatcaaa cagtgaaaag ggaatgataa gatgtatttt 2580
gaatgaactg tttttctgt agactagctg agaaattgtt gacataaaat aaagaattga 2640
agaaacacat tttaccattt tgtgaattgt tctgaactta aatgtccact aaaacaactt 2700
agacttctgt ttgctaaatc tgtttctttt tctaatattc taaaaaaaaa aaaaaggttt 2760
<210> 49
<211> 690
<212> PRT
<213> Homo sapiens
<400> 49
Met Lys Arq Leu Pro Leu Leu Val Val Phe Ser Thr Leu Leu Asn Cys
                 5
Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys
                                25
Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln
                85
Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
           100
                               105
Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
       115
                           120
Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
   130
                       135
Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile
Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Leu Leu Gly Tyr Lys
               165
                                   170
                                                      175
```

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

			180					185					190		
Glu	Phe	Val 195	Lys	Thr	Val	Asn	Asn 200	Phe	Val	Gln	Arg	Asp 205	Thr	Phe	Val
Val	Trp 210	Asp	Lys	Leu	Ser	Val 215	Asn	His	Arg	Arg	Thr 220	His	Leu	Thr	Lys
Leu 225	Met	His	Thr	Val	Glu 230	Gln	Ala	Thr	Leu	Arg 235	Ile	Ser	Gln	Ser	Phe 240
Gln	Lys	Thr	Thr	Glu 245	Phe	Asp	Thr	Asn	Ser 250	Thr	Asp	Ile	Ala	Leu 255	Lys
Val	Phe	Phe	Phe 260	Asp	Ser	Tyr	Asn	Met 265	Lys	His	Ile	His	Pro 270	His	Met
Asn	Met	Asp 275	Gly	Asp	Tyr	Ile	Asn 280	Ile	Phe	Pro	Lys	Arg 285	Lys	Ala	Ala
Tyr	Asp 290	Ser	Asn	Gly	Asn	Val 295	Ala	Val	Ala	Phe	Leu 300	Tyr	Tyr	Lys	Ser
Ile 305	Gly	Pro	Leu	Leu	Ser 310	Ser	Ser	Asp	Asn	Phe 315	Leu	Leu	Lys	Pro	Glr. 320
Asn	Tyr	Asp	Asn	Ser 325	Glu	Glu	Glu	Glu	Arg 330	Val	Ile	Ser	Ser	Val 335	Ile
Ser	Val	Ser	Met 340	Ser	Ser	Asn	Pro	Pro 345	Thr	Leu	Tyr	Glu	Leu 350	Glu	Lys
Ile	Thr	Phe 355	Thr	Leu	Ser	His	Arg 360	Lys	Val	Thr	Asp	Arg 365	Tyr	Arg	Ser
Leu	Cys 370	Ala	Phe	Trp	Asn	Tyr 375	Ser	Pro	Asp	Thr	Met 380	Asn	Gly	Ser	Trp
Ser 385	Ser	Glu	Gly	Cys	Glu 390	Leu	Thr	Tyr	Ser	Asn 395	Glu	Thr	His	Thr	Ser 400
Cys	Arg	Cys	Asn	His 405	Leu	Thr	His	Phe	Ala 410	Ile	Leu	Met	Ser	Ser 415	Gly
Pro	Ser	Ile	Gly 420	Ile	Lys	Asp	Tyr	Asn 425	Ile	Leu	Thr	Arg	Ile 430	Thr	Glr
Leu	Gly	Ile 435	Ile	Ile	Ser	Leu	Ile 440	Cys	Leu	Ala	Ile	Cys 445	Ile	Phe	Thr
Phe	Trp	Phe	Phe	Ser	Glu	Ile 455	Gln	Ser	Thr	Arg	Thr	Thr	Ile	His	Lys

Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly 465 470 475 480

Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu 485 490 495

Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly 500 505 510

Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe 515 520 525

Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val 530 540

Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys 545 550 555 560

Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly 565 570 575

Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile 580 585 590

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser 595 600 605

Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu 610 615 620

Phe Leu Leu Gly Thr Trp Ile Phe Gly Val Leu His Val Val His 625 630 635 640

Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln 645 650 655

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln 660 665 670

Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys 675 680 685

Leu Arg 690

<210> 50

<211> 589

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (61)

```
<223> a, t, c or g
<400> 50
tqqaaacata tcctccctca tatqaatatq qatqqaqact acataaatat atttccaaag 60
ngaaaagccg gcatatggat tcaaatggca atgttgcagt tgcattttta tattataaga 120
qtattqqtcc ctttqctttc atcatctqac aacttcttat tgaaacctca aaattatgat 180
aattctgaag aggaggaaag agtcatatct tcagtaattt cagtctcaat gagctcaaac 240
ccacccacat tatatgaact tgaaaaaata acatttacat taagtcatcg aaaggtcaca 300
gataggtata ggagtctatg tggcattttg gaatactcac ctgataccat gaatggcagc 360
tggtcttcag agggctgtga gctgacatac tcaaatgaga cccacacctc atgccgctgt 420
aatcacctga cacattttgc aattttgatg tcctctggtc cttccattgg tattaaagat 480
tataatattc ttacaaggat cactcaacta ggaataatta tttcactgat ttgtcttgcc 540
                                                                   589
atatgcattt ttaccttctg gttcttcagt gaaattcaaa gcaccagga
<210> 51
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 51
                                                                   20
ggtaatgagc tccattacag
<210> 52
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 52
                                                                   18
ggagtagaaa gcgcatgg
<210> 53
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 53
                                                                   22
cacctgatac catgaatggc ag
<210> 54
<211> 18
<212> DNA
```

<213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 54 cgagctcgaa ttaattcg	18
<210> 55 <211> 18 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 55 ggatctcctg agctcagg	18
<210> 56 <211> 23 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 56 cctagttgag tgatccttgt aag	23
<210> 57 <211> 50 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 57 atgagaccca cacctcatgc cgctgtaatc acctgacaca ttttgcaatt	50
<210> 58 <211> 2137 <212> DNA <213> Homo sapiens	
<400> 58 gctcccagcc aagaacctcg gggccgctgc gcggtgggga ggagttcccc gaaacccggc	

```
gggacaagaa gccgccgcct gcctgcccgg gcccggggag ggggctgggg ctggggccgg 180
aggeggggtg tgagtgggtg tgtgeggggg geggaggett gatgeaatee egataagaaa 240
tgctcgggtg tcttgggcac ctacccgtgg ggcccgtaag gcgctactat ataaggctgc 300
eggeeeggag eegeegeee gteagageag gagegetgeg teeaggatet agggeeaega 360
ccatcccaac ccggcactca cagccccgca gcgcatcccg gtcgccgccc agcctcccgc 420
acceccated ecddadetde decdadadee ceaggdaddt decatdedda geggdtdt 480
ggtggtccac gtatggatcc tggccggcct ctggctggcc gtggccgggc gccccctcgc 540
cttctcggac gcggggcccc acgtgcacta cggctggggc gaccccatcc gcctgcggca 600
cctqtacacc tccggccccc acgggctctc cagctgcttc ctgcgcatcc gtgccgacgg 660
cgtcgtggac tgcgcgcggg gccagagcgc gcacagtttg ctggagatca aggcagtcgc 720
tetqeqqaee qtqqeeatca agggegtgea cagegtgegg taeetetgea tgggegeega 780
cggcaagatg caggggctgc ttcagtactc ggaggaagac tgtgctttcg aggaggagat 840
ccgcccagat ggctacaatg tgtaccgatc cgagaagcac cgcctcccgg tctccctgag 900
cagtgccaaa cagcggcagc tgtacaagaa cagaggcttt cttccactct ctcatttcct 960
geccatgetg cecatggtee cagaggagee tgaggacete aggggeeact tggaatetga 1020
catgttetet tegeceetgg agacegacag catggaceca tttgggettg teaecggact 1080
ggaggccgtg aggagtccca gctttgagaa gtaactgaga ccatgcccgg gcctcttcac 1140
tgctgccagg ggctgtggta cctgcagcgt gggggacgtg cttctacaag aacagtcctg 1200
agtccacqtt ctqtttaqct ttaqqaaqaa acatctaqaa qttqtacata ttcaqagttt 1260
tecattqqca qtqccaqttt ctaqccaata qacttqtctq atcataacat tgtaagcctg 1320
tagettqccc agetqctqcc tqqqccccca ttetgctccc tcgaggttgc tggacaagct 1380
getgeactgt etcagttetg ettgaatace tecategatg gggaacteae tteetttgga 1440
aaaattetta tgteaagetg aaatteteta atttttete ateaetteee caggageage 1500
cagaagacag gcagtagttt taatttcagg aacaggtgat ccactctgta aaacagcagg 1560
taaatttcac tcaaccccat qtqqqaattq atctatatct ctacttccag ggaccatttg 1620
cccttcccaa atccctccaq qccaqaactq actggagcag gcatggccca ccaggcttca 1680
ggagtagggg aagcetggag ecceaeteea geeetgggae aaettgagaa tteeeeetga 1740
ggccagttct gtcatggatg ctgtcctgag aataacttgc tgtcccggtg tcacctgctt 1800
ccatctccca gcccaccagc cctctgccca cctcacatgc ctccccatgg attggggcct 1860
cccaqqcccc ccaccttatq tcaacctqca cttcttgttc aaaaaatcagg aaaagaaaag 1920
atttgaagac cccaagtctt gtcaataact tgctgtgtgg aagcagcggg ggaagaccta 1980
gaaccettte eccageactt ggttttecaa catgatattt atgagtaatt tattttgata 2040
tgtacatctc ttattttctt acattattta tgcccccaaa ttatatttat gtatgtaagt 2100
                                                                  2137
qaqqtttqtt ttqtatatta aaatggagtt tgtttgt
<210> 59
<211> 216
<212> PRT
<213> Homo sapiens
<400> 59
```

Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu 1

Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro 25

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr 35

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala 50

Asp 65	Gly	Val	Val	Asp	Cys 70	Ala	Arg	Gly	Gln	Ser 75	Ala	His	Ser	Leu	Leu 80	
Glu	Ile	Lys	Ala	Val 85	Ala	Leu	Arg	Thr	Val 90	Ala	Ile	Lys	Gly	Val 95	His	
Ser	Val	Arg	Tyr 100	Leu	Cys	Met	Gly	Ala 105	Asp	Gly	Lys	Met	Gln 110	Gly	Leu	
Leu	Gln	Tyr 115	Ser	Glu	Glu	Asp	Cys 120	Ala	Phe	Glu	Glu	Glu 125	Ile	Arg	Pro	
Asp	Gly 130	Tyr	Asn	Val	Tyr	Arg 135	Ser	Glu	Lys	His	Arg 140	Leu	Pro	Val	Ser	
Leu 145	Ser	Ser	Ala	Lys	Gln 150	Arg	Gln	Leu	Tyr	Lys 155	Asn	Arg	Gly	Phe	Leu 160	
Pro	Leu	Ser	His	Phe 165	Leu	Pro	Met	Leu	Pro 170	Met	Val	Pro	Glu	Glu 175	Pro	
Glu	Asp	Leu	Arg 180	Gly	His	Leu	Glu	Ser 185	Asp	Met	Phe	Ser	Ser 190	Pro	Leu	
Glu	Thr	Asp 195	Ser	Met	Asp	Pro	Phe 200	Gly	Leu	Val	Thr	Gly 205	Leu	Glu	Ala	
Val	Arg 210	Ser	Pro	Ser	Phe	Glu 215	Lys									
<212 <212	0> 60 L> 20 2> DI B> At	S NA	icia	l Sed	quen	ce										
<220 <220	3 > De		iptio nucle				cial	Seq	ience	e: Sy	ynthe	etic				
)> 60 cgcco		atgg	ctaca	aa t	gtgta	a									26
<212 <212	0> 6: L> 4: 2> DI 3> A:	2 NA	icia	l Sed	quen	ce										
<220 <220	3 > De		iptionucle				cial	Seq	uence	e: Sy	ynthe	etic				
)> 6:		at aa	ntgad	ac ac	atace	caaa	c ago	gaad	aata	ta					42

```
<210> 62
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
     oligonucleotide probe
<400> 62
                                                                22
ccagtccggt gacaagccca aa
<210> 63
<211> 1295
<212> DNA
<213> Homo sapiens
<400> 63
cccaqaaqtt caaqqqccc cqqcctcctq cqctcctqcc qccqqqaccc tcqacctcct 60
cagageagec ggctgccgcc ccgggaagat ggcgaggagg agccgccacc gcctcctcct 120
getgetgetg egetacetgg tggtegecet gggetateat aaggeetatg ggttttetge 180
cccaaaagac caacaagtag tcacagcagt agagtaccaa gaggctattt tagcctgcaa 240
aaccccaaaq aaqactqttt cctccaqatt aqaqtqqaaq aaactqqqtc qqaqtqtctc 300
ctttqtctac tatcaacaqa ctcttcaaqq tqattttaaa aatcqaqctg agatgataga 360
tttcaatatc cggatcaaaa atgtgacaag aagtgatgcg gggaaatatc gttgtgaagt 420
tagtgcccca tctgagcaag gccaaaacct ggaagaggat acagtcactc tggaagtatt 480
agtggctcca gcagttccat catgtgaagt accetettet getetgagtg gaactgtggt 540
agagctacga tgtcaagaca aagaagggaa tccagctcct gaatacacat ggtttaagga 600
tggcatccgt ttgctagaaa atcccagact tggctcccaa agcaccaaca gctcatacac 660
aatgaataca aaaactggaa ctctgcaatt taatactgtt tccaaactgg acactggaga 720
atatteetqt qaaqeeeqea attetqttgg atategeagg tgteetggga aacgaatgea 780
aqtaqatqat ctcaacataa qtggcatcat agcagccgta gtagttgtgg ccttagtgat 840
ttccgtttgt ggccttggtg tatgctatgc tcagaggaaa ggctactttt caaaagaaac 900
ctccttccag aagagtaatt cttcatctaa agccacgaca atgagtgaaa atgtgcagtg 960
gctcacgcct gtaatcccag cactttggaa ggccgcggcg ggcggatcac gaggtcagga 1020
gttctagacc agtctggcca atatggtgaa accccatctc tactaaaata caaaaattag 1080
ctgggcatgg tggcatgtgc ctgcagttcc agctgcttgg gagacaggag aatcacttga 1140
accegggagg eggaggttge agtgagetga gateaegeea etgeagteea geetgggtaa 1200
1295
tgtagaattc ttacaataaa tatagcttga tattc
<210> 64
<211> 312
<212> PRT
<213> Homo sapiens
<400> 64
Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Leu Arg Tyr
Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro
```

- Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu 35 40 45
- Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys
 50 55 60
- Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln
 65 70 75 80
- Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile 85 90 95
- Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser 100 105 110
- Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu 115 120 125
- Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser 130 135 140
- Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly
 145 150 155 160
- Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu 165 170 175
- Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met 180 185 190
- Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp 195 200 205
- Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg 210 215 220
- Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile 225 230 235 240
- Ile Ala Ala Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu 245 250 255
- Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser 260 265 270
- Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn 275 280 285
- Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala 290 295 300
- Gly Gly Ser Arg Gly Gln Glu Phe

```
305
                    310
<210> 65
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 65
                                                                   22
atcgttgtga agttagtgcc cc
<210> 66
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 66
                                                                   23
acctgcgata tccaacagaa ttg
<210> 67
<211> 48
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 67
ggaagaggat acagtcactc tggaagtatt agtggctcca gcagttcc
                                                                   48
<210> 68
<211> 2639
<212> DNA
<213> Homo sapiens
<400> 68
gacatcggag gtgggctagc actgaaactg cttttcaaga cgaggaagag gaggagaaag 60
agaaagaaga ggaagatgtt gggcaacatt tatttaacat gctccacagc ccggaccctg 120
gcatcatgct gctattcctg caaatactga agaagcatgg gatttaaata ttttacttct 180
aaataaatga attactcaat ctcctatgac catctataca tactccacct tcaaaaagta 240
catcaatatt atatcattaa ggaaatagta accttctctt ctccaatatg catgacattt 300
ttggacaatg caattgtggc actggcactt atttcagtga agaaaaactt tgtggttcta 360
tggcattcat catttgacaa atgcaagcat cttccttatc aatcagctcc tattgaactt 420
actagcactg actgtggaat ccttaagggc ccattacatt tctgaagaag aaagctaaga 480
tgaaggacat gccactccga attcatgtgc tacttggcct agctatcact acactagtac 540
```

```
aagotgtaga taaaaaaqtq gattqtocao ggttatgtao gtgtgaaato aggoottggt 600
ttacacccaq atccatttat atqqaaqcat ctacaqtqqa ttgtaatgat ttaggtcttt 660
taactttccc aqccaqattq ccaqctaaca cacaqattct tctcctacag actaacaata 720
ttgcaaaaat tgaatactcc acagactttc cagtaaacct tactggcctg gatttatctc 780
aaaacaattt atcttcagtc accaatatta atgtaaaaaa gatgcctcag ctcctttctg 840
tgtacctaga qqaaaacaaa cttactqaac tgcctgaaaa atgtctgtcc gaactgagca 900
acttacaaga actctatatt aatcacaact tgctttctac aatttcacct ggagccttta 960
ttggcctaca taatcttctt cgacttcatc tcaattcaaa tagattgcag atgatcaaca 1020
gtaagtggtt tgatgctctt ccaaatctag agattctgat gattggggaa aatccaatta 1080
tcagaatcaa agacatgaac tttaagcctc ttatcaatct tcgcagcctg gttatagctg 1140
gtataaacct cacagaaata ccagataacg ccttggttgg actggaaaac ttagaaagca 1200
tetettttta egataacagg ettattaaag taceceatgt tgetetteaa aaagttgtaa 1260
atctcaaatt tttggatcta aataaaaatc ctattaatag aatacgaagg ggtgatttta 1320
gcaatatgct acacttaaaa gagttgggga taaataatat gcctgagctg atttccatcg 1380
atagtettge tgtggataac etgecagatt taagaaaaat agaagetaet aacaaceeta 1440
gattqtctta cattcacccc aatqcatttt tcaqactccc caaqctqqaa tcactcatqc 1500
tgaacagcaa tgctctcagt gccctgtacc atggtaccat tgagtctctg ccaaacctca 1560
aggaaatcag catacacagt aaccccatca ggtgtgactg tgtcatccgt tggatgaaca 1620
tqaacaaaac caacattcqa ttcatqqagc caqattcact gttttgcgtg gacccacctq 1680
aattccaaqq tcaqaatqtt cqqcaaqtqc atttcaggga catqatggaa atttqtctcc 1740
ctcttatage teetgagage ttteetteta atctaaatgt agaagetggg agetatgttt 1800
cettteactg tagagetact geagaaceae ageetgaaat etactggata acacettetg 1860
gtcaaaaact cttgcctaat accetgacag acaagttcta tgtccattct gagggaacac 1920
tagatataaa tggcgtaact cccaaagaag ggggtttata tacttgtata gcaactaacc 1980
tagttggcgc tgacttgaag tctgttatga tcaaagtgga tggatctttt ccacaagata 2040
acaatggctc tttgaatatt aaaataagag atattcaggc caattcagtt ttggtgtcct 2100
ggaaagcaag ttctaaaatt ctcaaatcta gtgttaaatg gacagccttt gtcaagactg 2160
aaaattetea tgetgegeaa agtgetegaa taccatetga tgteaaggta tataatetta 2220
ctcatctgaa tccatcaact gagtataaaa tttgtattga tattcccacc atctatcaga 2280
aaaacagaaa aaaatgtgta aatgtcacca ccaaaggttt gcaccctgat caaaaagagt 2340
atgaaaagaa taataccaca acacttatgg cctgtcttgg aggccttctg gggattattg 2400
gtgtgatatg tettateage tgeetetete cagaaatgaa etgtgatggt ggaeaeaget 2460
atgtgaggaa ttacttacag aaaccaacct ttgcattagg tgagctttat cctcctctga 2520
taaatetetg ggaageagga aaagaaaaaa gtacateaet gaaagtaaaa gcaaetgtta 2580
taggtttacc aacaaatatg tootaaaaac caccaaggaa acctactcca aaaatgaac 2639
<210> 69
<211> 708
<212> PRT
<213> Homo sapiens
```

<400> 69

Met Lys Asp Met Pro Leu Arq Ile His Val Leu Gly Leu Ala Ile

Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu

Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met 35

Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro 55 60

- Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Gln Thr Asn Asn 65 70 75 80
- Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly 85 90 95
- Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val 100 105 110
- Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu 115 120 125
- Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu 130 135 140
- Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe 145 150 155 160
- Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu 165 170 175
- Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile 180 185 190
- Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe 195 200 205
- Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu 210 215 220
- Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser 225 230 235 240
- Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu 245 250 255
- Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile 260 265 270
- Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu 275 280 285
- Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala 290 295 300
- Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro 305 310 315 320
- Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu 325 330 335
- Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

			340					345					350		
Thr	Ile	Glu 355	Ser	Leu	Pro	Asn	Leu 360	Lys	Glu	Ile	Ser	Ile 365	His	Ser	Asr
Pro	Ile 370	Arg	Cys	Asp	Cys	Val 375	Ile	Arg	Trp	Met	Asn 380	Met	Asn	Lys	Thi
Asn 385	Ile	Arg	Phe	Met	Glu 390	Pro	Asp	Ser	Leu	Phe 395	Cys	Val	Asp	Pro	Pro 400
Glu	Phe	Gln	Gly	Gln 405	Asn	Val	Arg	Gln	Val 410	His	Phe	Arg	Asp	Met 415	Met
Glu	Ile	Суѕ	Leu 420	Pro	Leu	Ile	Ala	Pro 425	Glu	Ser	Phe	Pro	Ser 430	Asn	Let
Asn	Val	Glu 435	Ala	Gly	Ser	Tyr	Val 440	Ser	Phe	His	Cys	Arg 445	Ala	Thr	Ala
Glu	Pro 450	Gln	Pro	Glu	Ile	Tyr 455	Trp	Ile	Thr	Pro	Ser 460	Gly	Gln	Lys	Leı
Leu 465	Pro	Asn	Thr	Leu	Thr 470	Asp	Lys	Phe	Tyr	Val 475	His	Ser	Glu	Gly	Th: 480
Leu	Asp	Ile	Asn	Gly 485	Val	Thr	Pro	Lys	Glu 490	Gly	Gly	Leu	Tyr	Thr 495	Cys
Ile	Ala	Thr	Asn 500	Leu	Val	Gly	Ala	Asp 505	Leu	Lys	Ser	Val	Met 510	Ile	Lys
Val	Asp	Gly 515	Ser	Phe	Pro	Gln	Asp 520	Asn	Asn	Gly	Ser	Leu 525	Asn	Ile	Lys
Ile	Arg 530	Asp	Ile	Gln	Ala	Asn 535	Ser	Val	Leu	Val	Ser 540	Trp	Lys	Ala	Sei
Ser 545	Lys	Ile	Leu	Lys	Ser 550	Ser	Val	Lys	Trp	Thr 555	Ala	Phe	Val	Lys	Th:
Glu	Asn	Ser	His	Ala 565	Ala	Gln	Ser	Ala	Arg 570	Ile	Pro	Ser	Asp	Val 575	Lys
Val	Tyr	Asn	Leu 580	Thr	His	Leu	Asn	Pro 585	Ser	Thr	Glu	Tyr	Lys 590	Ile	Cys
Ile	Asp	Ile 595	Pro	Thr	Ile	Tyr	Gln 600	Lys	Asn	Arg	Lys	Lys 605	Суз	Val	Ası
Val	Thr		Lys	Gly	Leu	His		Asp	Gln	Lys	Glu 620		Glu	Lys	Ası

<400> 71

```
Asn Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile
                                        635
625
                    630
Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp
                645
                                    650
Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala
                                                    670
                                665
Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys
        675
                            680
Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro
                                            700
                        695
Thr Asn Met Ser
705
<210> 70
<211> 1305
<212> DNA
<213> Homo sapiens
<400> 70
gcccgggact ggcgcaaggt gcccaagcaa ggaaagaaat aatgaagaga cacatgtgtt 60
agctgcagcc ttttgaaaca cgcaagaagg aaatcaatag tgtggacagg gctggaacct 120
ttaccacgct tgttggagta gatgaggaat gggctcgtga ttatgctgac attccagcat 180
gaatctggta gacctgtggt taacccgttc cctctccatg tgtctcctcc tacaaagttt 240
tgttcttatg atactgtgct ttcattctgc cagtatgtgt cccaagggct gtctttgttc 300
ttcctctggg ggtttaaatg tcacctgtag caatgcaaat ctcaaggaaa tacctagaga 360
tetteeteet gaaacagtet taetgtatet ggaeteeaat eagateacat etatteeeaa 420
tgaaattttt aaggacctcc atcaactgag agttctcaac ctgtccaaaa atggcattga 480
qtttatcqat qaqcatqcct tcaaaqqagt aqctgaaacc ttgcagactc tggacttgtc 540
cgacaatcgg attcaaagtg tgcacaaaaa tgccttcaat aacctgaagg ccagggccag 600
aattgccaac aacccctggc actgcgactg tactctacag caagttctga ggagcatggc 660
qtccaatcat gagacagccc acaacgtgat ctgtaaaacg tccgtgttgg atgaacatgc 720
tggcagacca ttcctcaatg ctgccaacga cgctgacctt tgtaacctcc ctaaaaaaac 780
taccqattat gccatgctgg tcaccatgtt tggctggttc actatggtga tctcatatgt 840
ggtatattat gtgaggcaaa atcaggagga tgcccggaga cacctcgaat acttgaaatc 900
cctqccaaqc aggcaqaaqa aagcaqatga acctgatgat attagcactg tggtatagtg 960
tccaaactqa ctqtcattqa qaaaqaaaqa aaqtaqtttq cqattqcagt agaaataagt 1020
gqtttacttc tcccatccat tgtaaacatt tgaaactttg tatttcagtt ttttttgaat 1080
tatgccactg ctgaactttt aacaacact acaacataaa taatttgagt ttaggtgatc 1140
caccccttaa ttgtaccccc gatggtatat ttctgagtaa gctactatct gaacattagt 1200
tagatccatc tcactattta ataatgaaat ttatttttt aatttaaaag caaataaaag 1260
cttaactttg aaccatggga aaaaaaaaaa aaaaaaaaa aaaca
<210> 71
<211> 259
<212> PRT
<213> Homo sapiens
```

Met Asn Leu Val Asp Leu Trp Leu Thr Arg Ser Leu Ser Met Cys Leu 1 5 10 15

Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser
20 25 30

Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val 35 40 45

Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro 50 55 60

Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro 65 70 75 80

Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser 85 90 95

Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala 100 105 110

Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val 115 120 125

His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn 130 135 140

Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met 145 150 155 160

Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val 165 170 175

Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala 180 185 190

Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val 195 200 205

Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr 210 215 220

Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys 225 230 235 240

Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser 245 250 255

Thr Val Val

<210> 72 <211> 2290

```
<212> DNA
<213> Homo sapiens
<400> 72
accgagccga gcggaccgaa ggcgccccg agatgcaggt gagcaagagg atgctggcgg 60
ggggcgtgag gagcatgccc agccccctcc tggcctgctg gcagcccatc ctcctgctgg 120
tgctgggcte agtgctgtca ggctcggcca cgggctgccc gccccgctgc gagtgctccg 180
cccaggaccg cgctgtgctg tgccaccgca agtgctttgt ggcagtcccc gagggcatcc 240
ccaccqaqac qcqcctqctq qacctaqqca agaaccqcat caaaacgctc aaccaggacg 300
aqttcqccaq cttcccqcac ctqqaqqaqc tqqaqctcaa cqaqaacatc gtqaqcqccg 360
tggagecegg egeetteaae aacetettea aeeteeggae getgggtete egeageaaee 420
qéctqaaqet cateceqeta qqeqtettea etqqeeteag caacetgace aageaggaca 480
tcaqcqaqaa caaqatcqtt atcctactqq actacatqtt tcaggacctg tacaacctca 540
aqtcactqqa qqttqqcqac aatqacctcq tctacatctc tcaccgcgcc ttcagcggcc 600
tcaacaqcct qqaqcaqctq acqctqqaqa aatqcaacct gacctccatc cccaccgagg 660
cgctgtccca cctgcacggc ctcatcgtcc tgaggctccg gcacctcaac atcaatgcca 720
teegggaeta eteetteaag aggetgtace gaeteaaggt ettggagate teecactgge 780
cctacttgga caccatgaca cccaactgcc tctacggcct caacctgacg tccctgtcca 840
tcacacactg caatctgacc gctgtgccct acctggccgt ccgccaccta gtctatctcc 900
getteeteaa eeteteetae aaceeeatea geaceattga gggeteeatg ttgeatgage 960
tgctccggct gcaggagatc cagctggtgg gcgggcagct ggccgtggtg gagccctatg 1020
ccttccgcgg cctcaactac ctgcgcgtgc tcaatgtctc tggcaaccag ctgaccacac 1080
tgqaqqaatc aqtcttccac tcggtgggca acctggagac actcatcctg gactccaacc 1140
cgctggcctg cgactgtcgg ctcctgtggg tgttccggcg ccgctggcgg ctcaacttca 1200
accggcagca gcccacgtgc gccacgcccg agtttgtcca gggcaaggag ttcaaggact 1260
tecetgatgt getactgeec aactaettea cetgeegeeg egeeegeate egggaeegea 1320
aggcccagca ggtgtttgtg gacgagggcc acacggtgca gtttgtgtgc cgggccgatg 1380
gcgacccgcc gcccgccatc ctctggctct caccccgaaa gcacctggtc tcagccaaga 1440
gcaatgggeg gctcacagtc ttccctgatg gcacgctgga ggtgcgctac gcccaggtac 1500
aggacaacgg cacgtacctg tgcatcgcgg ccaacgcggg cggcaacgac tccatgcccg 1560
cccacctgca tgtgcgcagc tactcgcccg actggcccca tcagcccaac aagaccttcg 1620
ctttcatctc caaccagccg ggcgagggag aggccaacag caccegegcc actgtgcctt 1680
tccccttcga catcaagacc ctcatcatcg ccaccaccat gggcttcatc tctttcctgg 1740
qcqtcqtcct cttctqcctq qtqctqctqt ttctctqqaq ccggggcaaq ggcaacacaa 1800
agcacaacat cqaqatcqaq tatqtqcccc qaaaqtcqqa cgcaqgcatc agctccgccg 1860
acgcgccccg caagttcaac atgaagatga tatgaggccg gggcgggggg cagggacccc 1920
cgggcggccg ggcaggggaa ggggcctggt cgccacctgc tcactctcca gtccttccca 1980
cctcctccct acccttctac acacqttctc tttctccctc ccgcctccgt cccctgctgc 2040
cccccgccag ccctcaccac ctgccctcct tctaccagga cctcagaagc ccagacctqq 2100
ggaccccacc tacacagggg cattgacaga ctggagttga aagccgacga accgacacgc 2160
ggcagagtca ataattcaat aaaaaagtta cgaactttct ctgtaacttg ggtttcaata 2220
attatggatt tttatgaaaa cttgaaataa taaaaagaga aaaaaactaa aaaaaaaaa 2280
aaaaaaaaa
                                                                  2290
<210> 73
<211> 620
<212> PRT
<213> Homo sapiens
Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro
  1
                                     10
                                                         15
```

- Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly
 20 25 30
- Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys 35 40 45
- Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala 50 55 60
- Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys
 65 70 75 80
- Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His
 85 90 95
- Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro 100 105 110
- Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser 115 120 125
- Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn 130 135 140
- Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp 165 170 175
- Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser 180 185 190
- Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr
 195 200 205
- Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His 210 215 220
- Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg 225 230 235 240
- Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr 245 250 255
- Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His 260 265 270
- Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr 275 280 285
- Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly
 290 295 300

Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly 315 Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr 325 330 Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu 345 Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser 360 Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg 375 370 Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu 395 Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro 410 Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln 425 Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala 440 Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His 450 455 Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu 490 485 495 Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu 505 500 His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr 520 Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr 530

Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala

Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu

Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

570

575

565

	580	585	5	590	
Ile Glu Ile 595	Glu Tyr Val	Pro Arg Lys 600	s Ser Asp Ala	a Gly Ile S 605	er Ser
Ala Asp Ala 610	Pro Arg Lys	Phe Asn Met 615	Lys Met Ile 620		
<210> 74 <211> 22 <212> DNA <213> Artif	icial Sequenc	e			
	ription of Art onucleotide pr		quence: Syntl	netic	
<400> 74 tcacctggag	cctttattgg cc	!			22
<210> 75 <211> 23 <212> DNA <213> Artif	icial Sequenc	ee			
	ription of Art onucleotide pr		quence: Synt	netic	
<400> 75 ataccagcta	taaccagget ge	g			23
<210> 76 <211> 52 <212> DNA <213> Artif	ficial Sequenc	ee			
	ription of Art onucleotide pr		quence: Synt	hetic	
<400> 76 caacagtaag gg	tggtttgatg ct	cttccaaa to	ctagagatt ct	gatgattg	50 52
<210> 77 <211> 22 <212> DNA <213> Artif	Ficial Sequenc	ee			
	ription of Art		quence: Synt	hetic	

<400> 77 ccatgtgtct cctcctacaa ag	22
<210> 78 <211> 23 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 78 gggaatagat gtgatctgat tgg	23
<210> 79 <211> 50 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 79 cacctgtagc aatgcaaatc tcaaggaaat acctagagat cttcctcctg	50
<210> 80 <211> 22 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 80 agcaaccgcc tgaagctcat cc	22
<210> 81 <211> 24 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 81 aaggcgcggt gaaagatgta gacg	24
∠210× 82	

```
<211> 50
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
 <400> 82
 qactacatqt ttcaqqacct qtacaacctc aaqtcactqq aggttggcga
                                                                 50
 <210> 83
 <211> 1685
 <212> DNA
 <213> Homo sapiens
 <400> 83
cccacgcgtc cgcacctcgg ccccgggctc cgaagcggct cggggggcgcc ctttcggtca 60
acategtagt ccacecete eccatececa geeceegggg atteaggete geeagegeee 120
agccagggag ccggccggga agcgcgatgg gggccccagc cgcctcgctc ctgctcctgc 180
 tectgetgtt egeetgetge tgggegeeeg geggggeeaa eeteteeeag gaegaeagee 240
agccctggac atctgatgaa acagtggtgg ctggtggcac cgtggtgctc aagtgccaag 300
tgaaagatca cgaggactca tccctgcaat ggtctaaccc tgctcagcag actctctact 360
ttggggagaa gagagccctt cgagataatc gaattcagct ggttacctct acgccccacg 420
ageteageat eageateage aatgtggeee tggeagaega gggegagtae acetgeteaa 480
tetteactat qeetqtqeqa actqccaaqt ceeteqteac tqtqctagga attccacaga 540
agcccatcat cactggttat aaatcttcat tacgggaaaa agacacagcc accctaaact 600
gtcagtcttc tgggagcaag cctgcagccc ggctcacctg gagaaagggt gaccaagaac 660
tecacqqaqa accaaeceqe atacaqqaaq ateccaatqq taaaaectte actgteagea 720
gctcggtgac attccaggtt acccgggagg atgatggggc gagcatcgtg tgctctgtga 780
 accatgaatc tctaaaggga gctgacagat ccacctctca acgcattgaa gttttataca 840
 caccaactgc gatgattagg ccagaccctc cccatcctcg tgagggccag aagctgttgc 900
 tacactgtga gggtcgcggc aatccagtcc cccagcagta cctatgggag aaggaggca 960
gtgtgccacc cctgaagatg acccaggaga gtgccctgat cttccctttc ctcaacaaga 1020
gtgacagtgg cacctacggc tgcacagcca ccagcaacat gggcagctac aaggcctact 1080
 acacceteaa tgttaatgae eecagteegg tgeeeteete etecageace taccaegeea 1140
 teateggtgg gategtgget tteattgtet teetgetget cateatgete atetteettg 1200
gccactactt gatccggcac aaaggaacct acctgacaca tgaggcaaaa ggctccgacg 1260
 atgctccaga cgcggacacg gccatcatca atgcagaagg cgggcagtca ggaggggacg 1320
 acaagaagga atatttcatc tagaggcgcc tgcccacttc ctgcgccccc caggggccct 1380
gtggggactg ctggggccgt caccaacccg gacttgtaca gagcaaccgc agggccgccc 1440
 etcccgcttg ctccccagec cacccacec cctgtacaga atgtctgctt tgggtgcggt 1500
 ccctttccqt qqcttctctq catttqqqtt attattattt ttqtaacaat cccaaatcaa 1620
 atctgtctcc aggctggaga ggcaggagcc ctggggtgag aaaagcaaaa aacaaacaaa 1680
                                                                 1685
 aaaca
 <210> 84
 <211> 398
 <212> PRT
 <213> Homo sapiens
 <400> 84
```

- Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Leu Phe Ala 1 5 10 15
- Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln 20 25 30
- Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu
 35 40 45
- Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn 50 60
- Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp 65 70 75 80
- Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser 85 90 95
- Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile 100 105 110
- Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly
 115 120 125
- Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu 130 135 140
- Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala 145 150 155 160
- Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro 165 170 175
- Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser 180 185 190
- Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val 195 200 205
- Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser 210 215 220
- Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp 225 230 235 240
- Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu His Cys Glu Gly
 245 250 255
- Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser 260 265 270
- Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe 275 280 285

	Asn 290	Lys	Ser	Asp	Ser	Gly 295	Thr	Tyr	Gly	Cys	Thr 300	Ala	Thr	Ser	Asn	
Met 305	Gly	Ser	Tyr	Lys	Ala 310	Tyr	Tyr	Thr	Leu	Asn 315	Val	Asn	Asp	Pro	Ser 320	
Pro	Val	Pro	Ser	Ser 325	Ser	Ser	Thr	Tyr	His 330	Ala	Ile	Ile	Gly	Gly 335	Ile	
Val	Ala	Phe	Ile 340	Val	Phe	Leu	Leu	Leu 345	Ile	Met	Leu	Ile	Phe 350	Leu	Gly	
His	Tyr	Leu 355	Ile	Arg	His	Lys	Gly 360	Thr	Tyr	Leu	Thr	His 365	Glu	Ala	Lys	
Gly	Ser 370	Asp	Asp	Ala	Pro	Asp 375	Ala	Asp	Thr	Ala	Ile 380	Ile	Asn	Ala	Glu	٠
Gly 385	Gly	Gln	Ser	Gly	Gly 390	Asp	Asp	Lys	Lys	Glu 395	Tyr	Phe	Ile			
<220 <223 <400	> 22 > DN > An > De ol	NA stifi escri	nucle	on of	E Art	cific robe	cial	Sequ	ience	e: Sy	ynthe	etic				2.7
gcta <210			ccaca	agaag	gc co	2										22
<211 <212	> 22	2														
<213			icial	l Sed	quen	ce										
<220 <223	> De		iptio nucle				cial	Seqı	ıence	e: Sy	ynthe	etic				
<400 aacc			gtcad	ccgaç	gc to	3										22
<210 <211 <212 <213	> 26 > DN	IA	icial	l Sec	quenc	ce										
<220 <223		escri	iptio	on of	E Art	cific	cial	Sequ	ience	e: Sy	ynthe	etic				

oligonucleotide probe

<400> 87 cctagcacag tgacgaggga cttggc	26
<210> 88 <211> 50 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 88 aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc	50
<210> 89 <211> 50 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 89 gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt	50
<210> 90 <211> 2755 <212> DNA <213> Homo sapiens	
gggggttagg gaggaaggaa tecacececa eeeececaaa eeetttett eteetteet geetteggae attggageae taaatgaact tgaattgtg etgtggggag eaggatggte getgttaett tgtgatgaga teggggatga attgeteget ttaaaaatge tgetttegat tetgttgetg gagacgtete tttgttttge egetggaaae gttacagggg acgtttgeaa agagaagate tgtteetgea atgagataga aggggaeeta eaegtagaet gtgaaaaaaa gggetteaca agtetgeage gttteaetge eeegaettee eagttttaee atttattet geatggeaat teeeteaete gaetttteee taatgagte getaaeettt ataatgeggt tàgtttgeae atggaaaaea atggettgea tgaaategt eeggggget tteetggget geagetggt aaaaggetge acateaaeaa eaacaagate eeggggget tteetggget tteetgggg etggaegate tggaatatet eeaggetgat tttaatttat taegagatat agaeeegggg geetteeagg aettgaaeaa getggaggtg eteattttaa atgaeaatet eateageae etaaeega aegtgtteea gtatgtgee ateaeeeae tegaeatete eateageae etgaaaaee tgeeetatga gaggtettg gageaaatee etggaatate eggagateetg etaagagata aceettggga etgeaeetg gatetgee eetggaaga atggetggaa aacatteeea agaatgeeet gateggeega gtggtetgeg aageeeeeae eagaetgag ggtaaagaee teaatgaaae eaeegaaeag gaettgtgee etttgaaaaa eegagtggat tetagteee eggegeeee tgeeeaagaa gagaeetttg etttgaaaaa eegagtggat tetagteee ettgaaaaa eegagtggat eegagaeeeeeae	120 180 240 300 360 420 480 540 600 660 720 780 840 900 960
cctgccaact cctttcaaga caaatgggca agaggatcat gccacaccag ggtctgctcc	1080

```
aaacggaggt acaaagatcc caggcaactg gcagatcaaa atcagaccca cagcagcgat 1140
agggacgggt agctccagga acaaaccctt agctaacagt ttaccctgcc ctgggggctg 1200
cagetgegae caeateecag ggtegggttt aaagatgaae tgeaacaaca ggaaegtgag 1260
cagettgget gatttgaage ceaaqetete taacqtgeaq gagettttee tacgagataa 1320
caagatccac agcatccgaa aatcqcactt tqtqqattac aagaacctca ttctgttgga 1380
tctgggcaac aataacatcg ctactgtaga gaacaacact ttcaagaacc ttttggacct 1440
caggtggcta tacatggata gcaattacct ggacacgctg tcccgggaga aattcgcggg 1500
gctgcaaaac ctagagtacc tgaacgtgga gtacaacgct atccagctca tcctcccggg 1560
cactttcaat gccatgccca aactgaggat cetcattete aacaacaace tgctgaggte 1620
cctgcctgtg gacgtgttcg ctggggtctc gctctctaaa ctcagcctgc acaacaatta 1680
cttcatgtac ctcccggtgg caggggtgct ggaccagtta acctccatca tccagataga 1740
cctccacgga aacccctggg agtgctcctg cacaattgtg cctttcaagc agtgggcaga 1800
acgettgggt teegaagtge tgatgagega ceteaagtgt gagaegeegg tgaacttett 1860
tagaaaggat ttcatgctcc tctccaatga cgagatctgc cctcagctgt acgctaggat 1920
ctcgcccacg ttaacttcgc acagtaaaaa cagcactggg ttggcggaga ccgggacgca 1980
ctccaactcc tacctagaca ccagcagggt gtccatctcg gtgttggtcc cgggactgct 2040
gctggtgttt gtcacctccq ccttcaccqt gqtqqqcatq ctcqtgttta tcctgaggaa 2100
ccgaaagcgg tccaagagac gagatgccaa ctcctccgcg tccgagatta attccctaca 2160
qacaqtctqt qactcttcct actqqcacaa tqqqccttac aacqcaqatq qqqcccacaq 2220
aqtqtatqac tqtqqctctc actcqctctc aqactaaqac cccaacccca ataggggagg 2280
gcagagggaa ggcgatacat cettececae egcaggcaee eegggggett gaggggegtg 2340
tacccaaatc cccgcgccat cagcctggat gggcataagt agataaataa ctgtgagctc 2400
gcacaaccga aagggcctga ccccttactt agctccctcc ttgaaacaaa gagcagactg 2460
tggagagetg ggagagegea gecagetege tetttgetga gageeeettt tgacagaaag 2520
cccagcacga ccctgctgga agaactgaca gtgccctcgc cctcggcccc ggggcctgtg 2580
gggttggatg ccgcggttct atacatatat acatatatcc acatctatat agagagatag 2640
atatetattt tteecetgtg gattageece gtgatggete eetgttgget acgeagggat 2700
gggcagttgc acgaaggcat gaatgtattg taaataagta actttgactt ctgac
<210> 91
<211> 696
<212> PRT
<213> Homo sapiens
<400> 91
Met Leu Leu Trp Ile Leu Leu Glu Thr Ser Leu Cys Phe Ala Ala
```

Gly Asn Val Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn

Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr 35 40

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe 55

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn 65 70 75

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu 85 90

- Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His
 100 105 110
- Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly
 115 120 125
- Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp 130 135 140
- Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile 145 150 155 160
- Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr
 165 170 175
- Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu 180 185 190
- Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu 195 200 205
- Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys 210 215 220
- Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val 225 230 235 240
- Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr 245 250 255
- Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro
 260 265 270
- Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr 275 280 285
- Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala 290 295 300
- Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg 305 310 315 320
- Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala 325 330 335
- Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly 340 345 350
- Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala 355 360 365
- Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp 370 375 380

Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn 390 Leu Ile Leu Leu Asp Leu Gly Asn Asn Ile Ala Thr Val Glu Asn 405 Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser 425 420 Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn 440 Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro 450 455 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu 485 490 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala 505 500 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly 520 Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala 530 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr 550 555 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu 565 570 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu 610 Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val 630 635 Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser 645 650

Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

	660				665					670			
Trp His Ası	-	Pro Ty	r Asn	Ala 680	Asp	Gly	Ala	His	Arg 685	Val	Tyr	Asp	
Cys Gly Ser 690	His	Ser Le	u Ser 695	Asp									
<210> 92 <211> 22 <212> DNA <213> Artis	ficial	Seque	nce										
<220> <223> Description	_	n of A otide		cial	Seqı	ience	e: S <u>y</u>	ynthe	etic				
<400> 92 gttggatctg	ggcaa	caata	ac										22
<210> 93 <211> 24 <212> DNA <213> Artis	Eicial	Seque	nce										
<220> <223> Desc: oligo	_	n of A otide		cial	Seqı	ience	e: Sy	ynthe	etic				
<400> 93 attgttgtgc	aggct	gagtt	taag										24
<210> 94 <211> 45 <212> DNA <213> Artis	Eicial	Seque	nce										
<220> <223> Description	_	n of A		cial	Seq	uence	e: Sy	ynthe	etic				
<400> 94 ggtggctata	catgg	atagc	aatta	cctgg	g aca	acgc	gtc	ccg	3 9				45
<210> 95 <211> 2226 <212> DNA <213> Homo	sapie	ns				-							
<400> 95 agtcgactgc gctgcaccgg tggccgctgg	gcctg	gcagc	gctcc	gcaca	a cat	ttc	ctgt	cgc	ggcct	caa	gggaa	actgt	120

```
gaggggaagg gagggggaac cgggttgggg aagccagctg tagagggcgg tgaccgcgct 240
ccagacacag ctctgcgtcc tcgagcggga cagatccaag ttgggagcag ctctgcgtgc 300
ggggcctcag agaatgaggc cggcgttcgc cctgtgcctc ctctggcagg cgctctggcc 360
cqqqccqqqc ggcqqcqaac accccactgc cqaccqtqct ggctqctcgg cctcgggggc 420
ctgctacagc ctgcaccacg ctaccatgaa gcggcaggcg gccgaggagg cctgcatcct 480
gcgaggtggg gcgctcagca ccgtgcgtgc gggcgccgag ctgcgcgctg tgctcgcgct 540
cctgcgggca ggcccagggc ccggaggggg ctccaaagac ctgctgttct gggtcgcact 600
ggagcgcagg cgttcccact gcaccctgga gaacgagcct ttgcggggtt tctcctggct 660
qtcctccgac cccggcggtc tcgaaagcga cacgctgcag tgggtggagg agccccaacg 720
ctcctgcacc gcgcggagat gcgcggtact ccaggccacc ggtggggtcg agcccgcagg 780
ctggaaggag atgcgatgcc acctgcgcgc caacggctac ctgtgcaagt accagtttga 840
ggtcttgtgt cctgcgccgc gccccggggc cgcctctaac ttgagctatc gcgcgccctt 900
ccagctgcac agcgccgctc tggacttcag tccacctggg accgaggtga gtgcgctctg 960
ccqqqqacaq ctcccqatct caqttacttg catcgcggac gaaatcggcg ctcgctggga 1020
caaactctcg ggcgatgtgt tgtgtccctg ccccgggagg tacctccgtg ctggcaaatg 1080
equagagete cetaactgee tagacgaett gggaggettt geetgegaat gtgetacggg 1140
cttcgagctg gggaaggacg gccgctcttg tgtgaccagt ggggaaggac agccgaccct 1200
tggggggacc ggggtgccca ccaggcgccc gccggccact gcaaccagcc ccgtgccgca 1260
gagaacatgg ccaatcaggg tcgacgagaa gctgggagag acaccacttg tccctgaaca 1320
agacaattca gtaacatcta ttcctgagat tcctcgatgg ggatcacaga gcacgatgtc 1380
taccetteaa atgteeette aageegagte aaaggeeact ateaceecat eagggagegt 1440
qatttccaaq tttaattcta cqacttcctc tgccactcct caggctttcg actcctcctc 1500
tgccgtggtc ttcatatttg tgagcacagc agtagtagtg ttggtgatct tgaccatgac 1560
agtactgggg cttgtcaagc tctgctttca cgaaagcccc tcttcccagc caaggaagga 1620
gtctatgggc ccgccgggcc tggagagtga tcctgagccc gctgctttgg gctccagttc 1680
tgcacattgc acaaacaatg gggtgaaagt cggggactgt gatctgcggg acagagcaga 1740
gggtgccttg ctggcggagt cccctcttgg ctctagtgat gcatagggaa acaggggaca 1800
tgggcactcc tgtgaacagt ttttcacttt tgatgaaacg gggaaccaag aggaacttac 1860
ttgtgtaact gacaatttct gcagaaatcc cccttcctct aaattccctt tactccactg 1920
aggagctaaa tcagaactgc acactccttc cctgatgata gaggaagtgg aagtgccttt 1980
aggatggtga tactggggga ccgggtagtg ctggggagag atattttctt atgtttattc 2040
qqaqaatttg qagaagtgat tgaacttttc aagacattgg aaacaaatag aacacaatat 2100
aatttacatt aaaaaataat ttctaccaaa atggaaagga aatgttctat gttgttcagg 2160
ctaggagtat attggttcga aatcccaggg aaaaaaataa aaataaaaaa ttaaaggatt 2220
                                                                  2226
gttgat
<210> 96
<211> 490
<212> PRT
<213> Homo sapiens
<400> 96
Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro
```

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln
35 40 45

Gly Pro Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser

25

20

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val 50 55 60 Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly

290

Pro Gly Pro Gly Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu 120 Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala 130 135 Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu 170 Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro 200 Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val 210 Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly 230 Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys 245 250 Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr 280

Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln

Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln

330

Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg

Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro

			340					345					350			
Ser	Thr	Met 355	Ser	Thr	Leu	Gln	Met 360	Ser	Leu	Gln	Ala	Glu 365	Ser	Lys	Ala	
Thr	Ile 370	Thr	Pro	Ser	Gly	Ser 375	Val	Ile	Ser	Lys	Phe 380	Asn	Ser	Thr	Thr	
Ser 385	Ser	Ala	Thr	Pro	Gln 390	Ala	Phe	Asp	Ser	Ser 395	Ser	Ala	Val	Val	Phe 400	
Ile	Phe	Val	Ser	Thr 405	Ala	Val	Val	Val	Leu 410	Val	Ile	Leu	Thr	Met 415	Thr	
Val	Leu	Gly	Leu 420	Val	Lys	Leu	Cys	Phe 425	His	Glu	Ser	Pro	Ser 430	Ser	Gln	
Pro	Arg	Lys 435	Glu	Ser	Met	Gly	Pro 440	Pro	Gly	Leu	Glu	Ser 445	Asp	Pro	Glu	
Pro	Ala 450	Ala	Leu	Gly	Ser	Ser 455	Ser	Ala	His	Cys	Thr 460	Asn	Asn	Gly	Val	
Lys 465	Val	Gly	Asp	Cys	Asp 470	Leu	Arg	Asp	Arg	Ala 475	Glu	Gly	Ala	Leu	Leu 480	
Ala	Glu	Ser	Pro	Leu 485	Gly	Ser	Ser	Asp	Ala 490							
<211 <212)> 9' -> 24 !> Di !> Ai	1	icia	l Sed	quenc	ce										
<220 <223	3> De	escri Ligor	_				cial	Seqı	ıence	e: Sy	ynthe	etic				
)> 9' lagga	7 aga t	gcga	atgc	ca co	ctg										24
<211 <212)> 98 .> 20 ?> Dî ?> Ai	כ	icia	l Sed	quenc	ce										
<220 <223	3 > De	escri Ligor	-				cial	Seqi	uence	e: Sy	ynthe	etic				
)> 98 cagt	gg g	ggaad	ggaca	ag											20

<210><211><211><212><213>	20	
<220> <223>	Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> acaga	99 gcaga gggtgccttg	20
<210><211><211><212><213>	24	
<220> <223>	Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> tcagg	100 gacaa gtggtgtctc tccc	24
<210><211><211><212><213>	24	
<220> <223>	Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> tcaggg	101 gaagg agtgtgcagt tctg	24
<210><211><212><212><213>	50	
<220> <223>	Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> acagct	102 coog atotoagtta ottgoatogo ggaogaaato ggogotogot	50
<210><211><212>	2026	

```
<400> 103
cggacgcgtg ggattcagca gtggcctgtg gctgccagag cagctcctca ggggaaacta 60
agogtogagt cagacggcac cataatogcc tttaaaagtg cotcogccot googgcogcg 120
tateceeegg etacetggge egeceegegg eggtgegege gtgagaggga gegegeggge 180
agcogagogo oggtgtgago cagogotgot gocagtgtga goggoggtgt gagogoggtg 240
ggtgcggagg ggcgtgtgtg ccggcgcgcg cgccgtgggg tgcaaacccc gagcgtctac 300
gctgccatga ggggcgcgaa cgcctgggcg ccactctgcc tgctgctggc tgccgccacc 360
cagetetege ggeageagte eccagagaga cetgttttea eatgtggtgg cattettaet 420
ggagagtctg gatttattgg cagtgaaggt tttcctggag tgtaccctcc aaatagcaaa 480
tgtacttgga aaatcacagt tcccgaagga aaagtagtcg ttctcaattt ccgattcata 540
gacctcgaga gtgacaacct gtgccgctat gactttgtgg atgtgtacaa tggccatgcc 600
aatggccagc gcattggccg cttctgtggc actttccggc ctggagccct tgtgtccagt 660
ggcaacaaga tgatggtgca gatgatttct gatgccaaca cagctggcaa tggcttcatg 720
gccatgttct ccgctgctga accaaacgaa agaggggatc agtattgtgg aggactcctt 780
gacagacett ceggetettt taaaaceece aactggecag acegggatta ceetgeagga 840
gtcacttgtg tgtggcacat tgtagcccca aagaatcagc ttatagaatt aaagtttgag 900
aaqtttqatq tqqaqcqaqa taactactgc cqatatgatt atgtggctgt gtttaatggc 960
ggggaagtca acgatgctag aagaattgga aagtattgtg gtgatagtcc acctgcgcca 1020
attqtqtctq aqaqaaatqa acttcttatt caqtttttat caqacttaag tttaactgca 1080
qatqqqttta ttqqtcacta catattcaqq ccaaaaaaac tgcctacaac tacagaacag 1140
cctqtcacca ccacattccc tgtaaccacq ggtttaaaac ccaccgtggc cttgtgtcaa 1200
caaaagtgta gacggacggg gactctggag ggcaattatt gttcaagtga ctttgtatta 1260
gccggcactg ttatcacaac catcactcgc gatgggagtt tgcacgccac agtctcgatc 1320
atcaacatct acaaagaggg aaatttggcg attcagcagg cgggcaagaa catgagtgcc 1380
aggetgactg tegtetgeaa geagtgeeet eteeteagaa gaggtetaaa ttacattatt 1440
atgggccaag taggtgaaga tgggcgaggc aaaatcatgc caaacagctt tatcatgatg 1500
ttcaaqacca agaatcagaa gctcctggat gccttaaaaa ataagcaatg ttaacagtga 1560
actgtgtcca tttaagctgt attctgccat tgcctttgaa agatctatgt tctctcagta 1620
qaaaaaaaaa tacttataaa attacatatt ctgaaagagg attccgaaag atgggactgg 1680
ttgactette acatgatgga ggtatgagge etecgagata getgagggaa gttetttgce 1740
tgctgtcaga ggagcagcta tctgattgga aacctgccga cttagtgcgg tgataggaag 1800
ctaaaagtgt caagcgttga cagcttggaa gcgtttattt atacatctct gtaaaaggat 1860
attttagaat tgagttgtgt gaagatgtca aaaaaagatt ttagaagtgc aatatttata 1920
gtgttatttg tttcaccttc aagcctttgc cctgaggtgt tacaatcttg tcttgcgttt 1980
tctaaatcaa tgcttaataa aatattttta aaggaaaaaa aaaaaa
<210> 104
<211> 415
<212> PRT
<213> Homo sapiens
<400> 104
Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Ala Ala
                                     10
Ala Thr Gln Leu Ser Arq Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
                                                     3.0
             20
                                 25
Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
```

- Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu 65 70 75 80
- Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly
 85 90 95
- His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro 100 105 110
- Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser 115 120 125
- Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala 130 135 140
- Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg 145 150 155 160
- Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro 165 170 175
- Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu 180 185 190
- Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys 195 200 205
- Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Glu Val Asn Asp Ala 210 215 220
- Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val 225 230 235 240
- Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu 245 250 255
- Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu 260 . 265 270
- Pro Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr 275 280 285
- Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr 290 295 300
- Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly 305 310 315 320
- Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val
 325 330 335
- Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

		340					345					350			
Gly L	ys As 35		Ser	Ala	Arg	Leu 360	Thr	Val	Val	Cys	Lys 365	Gln	Суѕ	Pro	
	eu Ar 70	g Arg	Gly	Leu	Asn 375	Tyr	Ile	Ile	Met	Gly 380	Gln	Val	Gly	Glu	
Asp G	ly Ar	g Gly	Lys	Ile 390	Met	Pro	Asn	Ser	Phe 395	Ile	Met	Met	Phe	Lys 400	,
Thr L	ys As	n Gln	Lys 405	Leu	Leu	Asp	Ala	Leu 410	Lys	Asn	Lys	Gln	Cys 415		
<210><211><211><212><213>	22 DNA	ficia.	l Se	quen	ce										
<220> <223>	Desc	ripti Jonucl				cial	Seq	uence	e: Sy	ynth	etic				
<400> ccgat		ı gacc	tcga	ga g	t										22
<210><211><211><212><213>	22 DNA	ficia.	l Se	quen	ce										
<220> <223>	Desc	ripti gonucl				cial	Seq	uence	e: S	ynth	etic				
<400> gtcaa		cctc	caca	at a	С										22
<210><211><211><212><213>	45 DNA	ficia.	ıl Se	quen	ce										
<220> <223>	Desc	ripti gonucl					Seq	uenc	e: S	ynth	etic				
<400> gtgta		g gcca	ıtgcc	aa t	ggcc	agcg	c at	tggc	cgct	tct	gt				45
<210><211><211>	1838	3													

<213> Homo sapiens

```
<400> 108
eggacgegtg ggeggaegeg tgggeggeec aeggegeeeg egggetgggg eggtegette 60
ttoottotoo gtggootaog agggtoocca gootgggtaa agatggoocc atggooccog 120
aagggeetag teecagetgt getetgggge etcageetet teetcaacet eecaggaeet 180
atotggetee agecetetee aceteeceag tetteteece egeeteagee ceateegtgt 240
catacctgcc ggggactggt tgacagcttt aacaagggcc tggagagaac catccgggac 300
aactttggag gtggaaacac tgcctgggag gaagagaatt tgtccaaata caaagacagt 360
gagacccgcc tggtagaggt gctggagggt gtgtgcagca agtcagactt cgagtgccac 420
cgcctgctgg agctgagtga ggagctggtg gagagctggt ggtttcacaa gcagcaggag 480
gccccggacc tettecagtg gctgtgctca gattecetga agetetgctg ccccgcagge 540
acctteggge cetectgeet tecetgteet gggggaacag agaggeeetg eggtggetae 600
gggcagtgtg aaggagaagg gacacgaggg ggcagcgggc actgtgactg ccaagccggc 660
tacgggggtg aggcctgtgg ccagtgtggc cttggctact ttgaggcaga acgcaacgcc 720
agecatetgg tatgttegge ttgttttgge eeetgtgeee gatgeteagg acetgaggaa 780
tcaaactgtt tgcaatgcaa gaagggctgg gccctgcatc acctcaagtg tgtagacatt 840
gatgagtgtg gcacagaggg agccaactgt ggagctgacc aattctgcgt gaacactgag 900
ggctcctatg agtgccgaga ctgtgccaag gcctgcctag gctgcatggg ggcagggcca 960
gqtcgctgta agaagtgtag ccctggctat cagcaggtgg gctccaagtg tctcgatgtg 1020
gatgagtgtg agacagaggt gtgtccggga gagaacaagc agtgtgaaaa caccgagggc 1080
ggttatcgct gcatctgtgc cgagggctac aagcagatgg aaggcatctg tgtgaaggag 1140
cagatcccag agtcagcagg cttcttctca gagatgacag aagacgagtt ggtggtgctg 1200
cagcagatgt tetttggeat catcatetgt geactggeca egetggetge taagggegae 1260
ttggtgttca ccgccatctt cattggggct gtggcggcca tgactggcta ctggttgtca 1320
gagcgcagtg accgtgtgct ggagggcttc atcaagggca gataatcgcg gccaccacct 1380
gtaggacete eteceaceca egetgeeece agagettggg etgeeeteet getggacaet 1440
caggacaget tggtttattt ttgagagtgg ggtaagcace cetacetgee ttacagagca 1500
gcccaggtac ccaggcccgg gcagacaagg cccctggggt aaaaagtagc cctgaaggtg 1560
gataccatga gctcttcacc tggcggggac tggcaggctt cacaatgtgt gaatttcaaa 1620
agtttttcct taatggtggc tgctagagct ttggcccctg cttaggatta ggtggtcctc 1680
acaggggtgg ggccatcaca gctccctcct gccagctgca tgctgccagt tcctgttctg 1740
tgttcaccac atccccacac cccattgcca cttatttatt catctcagga aataaagaaa 1800
                                                                  1838
ggtcttggaa agttaaaaaa aaaaaaaaa aaaaaaaa
```

```
<210> 109
```

<400> 109

```
Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
1 5 10 15
```

<211> 420

<212> PRT

<213> Homo sapiens

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser 20 25 30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
35 40 45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile 50 55 60

Arg Asp Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser 105 Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro 115 120 Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro 135 Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu 145 Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Glu Ala Cys 185 Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His 200 Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro 215 Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His 225 Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg 265 Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg 280 275 Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln 305 Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr 325 330

Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala 340 345 350

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln 355 360 365	
Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys 370 375 380	
Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met 385 390 395 400	
Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe 405 410 415	
Ile Lys Gly Arg 420	
<210> 110 <211> 50 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 110 cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga	50
<210> 111 <211> 22 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 111 attctgcgtg aacactgagg gc	22
<210> 112 <211> 22 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 112 atctgcttgt agccctcggc ac	22
<210> 113	

```
<211> 1616
<212> DNA
<213> Homo sapiens
<220>
<221> modified base
<222> (1461)
<223> a, t, c or g
<400> 113
tgagaccete etgeageett eteaagggae ageeceaete tgeetettge teeteeaggg 60
cagcaccatg cagcccctgt ggctctgctg ggcactctgg gtgttgcccc tggccagccc 120
cggggccgcc ctgaccgggg agcagctcct gggcagcctg ctgcggcagc tgcagctcaa 180
agaggtgccc accetggaca gggccgacat ggaggagetg gtcatcccca cccacgtgag 240
ggcccagtac gtggccctgc tgcagcgcag ccacggggac cgctcccgcg gaaagaggtt 300
caqccaqaqc ttccqaqaqq tqqccgqcag gttcctggcg ttggaggcca gcacacacct 360
qctqqtqttc qqcatqqaqc aqcqqctqcc qcccaacagc gagctggtgc aggccgtgct 420
geggetette eaggageegg teeceaagge egegetgeae aggeaeggge ggetgteece 480
qeqcaqeqee eqqqeeeqqq tqaeeqteqa qtqqetgege gteegegaeg aeggeteeaa 540
ccgcacctcc ctcatcgact ccaggctggt gtccgtccac gagagcggct ggaaggcctt 600
cgacgtgacc gaggccgtga acttctggca gcagctgagc cggccccggc agccgctgct 660
gctacaggtg teggtgcaga gggagcatet gggecegetg gegteeggeg eccacaaget 720
ggtccgcttt gcctcgcagg gggcgccagc cgggcttggg gagccccagc tggagctgca 780
caccetggae ettggggaet atggagetea gggegaetgt gaecetgaag caccaatgae 840
cqaqqqcacc cqctqctqcc gccaggagat gtacattgac ctgcagggga tgaagtgggc 900
cgagaactgg gtgctggagc ccccgggctt cctggcttat gagtgtgtgg gcacctgccg 960
geageeeceg gaggeeetgg cetteaagtg geegtttetg gggeetegae agtgeatege 1020
ctcggagact gactcgctgc ccatgatcgt cagcatcaag gagggaggca ggaccaggcc 1080
ccaqqtqqtc aqcctgccca acatgagggt gcagaagtgc agctgtgcct cggatggtgc 1140
gtgtgtgttt ctgaagtgtt cgagggtacc aggagagctg gcgatgactg aactgctgat 1260
ggacaaatgc tctgtgctct ctagtgagcc ctgaatttgc ttcctctgac aagttacctc 1320
acctaatttt tgcttctcag gaatgagaat ctttggccac tggagagccc ttgctcagtt 1380
ttctctattc ttattattca ctgcactata ttctaagcac ttacatgtgg agatactgta 1440
acctgagggc agaaagccca ntgtgtcatt gtttacttgt cctgtcactg gatctgggct 1500
aaagtcctcc accaccactc tggacctaag acctggggtt aagtgtgggt tgtgcatccc 1560
caatccagat aataaagact ttgtaaaaca tgaataaaac acattttatt ctaaaa
                                                                1616
<210> 114
<211> 366
<212> PRT
<213> Homo sapiens
<400> 114
Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala
Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu
            20
                                25
Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met
```

- Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu 50 55 60
- Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln 65 70 75 80
- Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr 85 90 95
- His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu 100 105 110
- Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala 115 120 125
- Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg 130 135 140
- Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr 145 150 155 160
- Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys 165 170 175
- Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg 180 185 190
- Pro Arg Gln Pro Leu Leu Gln Val Ser Val Gln Arg Glu His Leu 195 200 205
- Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln 210 215 220
- Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu 225 230 235 240
- Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro 245 250 255
- Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu 260 265 270
- Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe 275 280 285
- Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu 290 295 300
- Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu 305 310 315 320
- Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr 325 330 335

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser 340 345 350	
Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro 355 360 365	
<210> 115 <211> 21 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 115 aggactgcca taacttgcct g 21	
<210> 116 <211> 22 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 116 ataggagttg aagcagcgct gc 22	
<210> 117 <211> 45 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 117 tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc 45	
<210> 118 <211> 1857 <212> DNA <213> Homo sapiens	
<400> 118 gtctgttccc aggagtcctt cggcggctgt tgtgtcagtg gcctgatcgc gatggggaca 60 aaggcgcaag tcgagaggaa actgttgtgc ctcttcatat tggcgatcct gttgtgctcc 12 ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcagaat tcctgagaat 18	0

65

70

85

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe

```
aatcctgtga agttgtcctg tgcctactcg ggcttttctt ctccccgtgt ggagtggaag 240
tttqaccaaq qaqacaccac cagactcgtt tgctataata acaagatcac agcttcctat 300
gaqqaccqqq tqaccttctt qccaactggt atcaccttca agtccgtgac acgggaagac 360
actgggacat acacttgtat ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420
gtcaagctca tcgtgcttgt gcctccatcc aagcctacag ttaacatccc ctcctctgcc 480
accattggga accgggcagt gctgacatgc tcagaacaag atggttcccc accttctgaa 540
tacacctggt tcaaagatgg gatagtgatg cctacgaatc ccaaaagcac ccgtgccttc 600
agcaactett cetatgteet gaateeeaca acaggagage tggtetttga teeeetgtea 660
gcctctgata ctggagaata cagctgtgag gcacggaatg ggtatgggac acccatgact 720
tcaaatqctq tqcqcatqqa aqctqtqqag cggaatqtqq gggtcatcqt ggcagccqtc 780
cttgtaaccc tgattctcct gggaatcttg gtttttggca tctggtttgc ctatagccga 840
ggccactttg acagaacaaa gaaagggact tcgagtaaga aggtgattta cagccagcct 900
agtgcccgaa gtgaaggaga attcaaacag acctcgtcat tcctggtgtg agcctgqtcq 960
gctcaccgcc tatcatctgc atttgcctta ctcaggtgct accggactct ggcccctgat 1020
gtctgtagtt tcacaggatg ccttatttgt cttctacacc ccacagggcc ccctacttct 1080
teggatgtgt ttttaataat gteagetatg tgeeccatee teetteatge ceteceteec 1140
tttcctacca ctqctqaqtq qcctqqaact tqtttaaagt gtttattccc catttctttg 1200
agggatcagg aaggaateet gggtatgeea ttgaetteee ttetaagtag acageaaaaa 1260
tggcggggt cgcaggaatc tgcactcaac tgcccacctg gctggcaggg atctttgaat 1320
aggtatettq agettqqtte tqqqetettt cettqtqtac tqacqaccag ggccagetqt 1380
tctagagcgg gaattagagg ctagagcggc tgaaatggtt gtttggtgat gacactgggg 1440
tecttecate tetggggeee actetettet gtetteceat gggaagtgee actgggatee 1500
ctctgccctg tcctcctgaa tacaagctga ctgacattga ctgtgtctgt ggaaaatggg 1560
agctcttgtt gtggagagca tagtaaattt tcagagaact tgaagccaaa aggatttaaa 1620
accqctqctc taaaqaaaaq aaaactqgag gctgggcgca gtggctcacg cctgtaatcc 1680
cagaggetga ggeaggegga teacetgagg tegggagtte gggateagee tgaceaacat 1740
ggagaaaccc tactggaaat acaaagttag ccaggcatgg tggtgcatgc ctgtagtccc 1800
aqctqctcaq qaqcctqqca acaaqagcaa aactccagct caaaaaaaaa aaaaaaa
                                                                  1857
<210> 119
<211> 299
<212> PRT
<213> Homo sapiens
<400> 119
Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
  1
Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
                                 25
Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
         35
Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
```

75

90

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser 100 105 110

Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val 115 120 125

Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr 130 135 140

Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro 145 150 155 160

Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn 165 170 175

Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro 180 185 190

Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
195 200 205

Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser 210 220

Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val 225 230 235 240

Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly 245 250 255

Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly 260 265 270

Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu 275 280 285

Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val 290 295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 120

tcgcggagct gtgttctgtt tccc

<210> 121

<211> 50

<212> <213>	DNA Artificial Sequence	
	Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> tgatcg		50
<210><211><212><212><213>	20	
	Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> acacct		20
<210><211><212><213>	24	
	Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> taggaa		24
<210><211><212><213>	20	
	Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> ttgcct		20
<210><211><212><213>	20	
<220>	Description of Artificial Sequence: Synthetic	

oligonucleotide probe

```
<400> 125
                                                                  20
actcagcagt ggtaggaaag
<210> 126
<211> 1210
<212> DNA
<213> Homo sapiens
<400> 126
cagegegtgg ceggegeege tgtggggaea geatgagegg eggttggatg gegeaggttg 60
gagegtggeg aacagggget etgggeetgg egetgetget getgetegge eteggaetag 120
gcctggaggc cgccgcgagc ccgctttcca ccccgacctc tgcccaggcc gcaggcccca 180
gctcaggctc gtgcccaccc accaagttcc agtgccgcac cagtggctta tgcgtgcccc 240
tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtgca 300
ggattgagcc atgtacccag aaagggcaat gcccaccgcc ccctggcctc ccctgcccct 360
gcaccggcgt cagtgactgc tctgggggaa ctgacaagaa actgcgcaac tgcagccgcc 420
tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480
ggcgctgcga cggccaccca gactgtcccg actccagcga cgagctcggc tgtggaacca 540
atgagatect eceggaaggg gatgecacaa ecatggggee ecetgtgace etggagagtg 600
tcacctctct caggaatgcc acaaccatgg ggccccctgt gaccctggag agtgtcccct 660
ctgtcgggaa tgccacatcc tcctctgccg gagaccagtc tggaagccca actgcctatg 720
gggttattgc agctgctgcg gtgctcagtg caagcctggt caccgccacc ctcctccttt 780
tgtcctggct ccgagcccag gagcgcctcc gcccactggg gttactggtg gccatgaagg 840
agtecetget getgteagaa cagaagaeet egetgeeetg aggacaagea ettgeeacea 900
ccgtcactca gccctgggcg tagccggaca ggaggagagc agtgatgcgg atgggtaccc 960
qqqcacacca qccctcagag acctgagttc ttctggccac gtggaacctc gaacccgagc 1020
tcctgcagaa gtggccctgg agattgaggg tccctggaca ctccctatgg agatccgggg 1080
agctaggatg gggaacctgc cacagccaga actgaggggc tggccccagg cagctcccag 1140
ggggtagaac ggccctgtgc ttaagacact ccctgctgcc ccgtctgagg gtggcgatta 1200
                                                                   1210
aagttgcttc
<210> 127
<211> 282
<212> PRT
<213> Homo sapiens
<400> 127
Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala
  1
Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Glu
Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly
                                                  45
         35
                             40
Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
                         55
     50
Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys
                                         75
                     70
```

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln 85 90 95

Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly
100 105 110

Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Leu Arg Asn Cys Ser 115 120 125

Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp 130 135 140

Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp 145 150 155 160

Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly 165 170 175

Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser 180 185 190

Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val
195 200 205

Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly 210 215 220

Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Ala Val Leu Ser Ala 225 230 235 240

Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln 245 250 255

Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu 260 265 270

Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro 275 280

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 128
aagttccagt gccgcaccag tggc

```
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 129
ttggttccac agccgagctc gtcg
                                                                   24
<210> 130
<211> 50
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 130
                                                                   50
gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc
<210> 131
<211> 1843
<212> DNA
<213> Homo sapiens
<220>
<221> modified_base
<222> (1837)
<223> a, t, c or g
<400> 131
cccaegegte eggteteget egetegegea geggeggeag eagaggtege geacagatge 60
gggttagact ggcggggga ggaggcggag gagggaagga agctgcatgc atgagaccca 120
cagactettg caagetggat geeetetgtg gatgaaagat gtateatgga atgaaceega 180
gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240
gactettgge egtgateetg tggttteage tggegetgtg etteggeeet geacagetea 300
cgggcgggtt cgatgacctt caagtgtgtg ctgaccccgg cattcccgag aatggcttca 360
ggacccccag cggaggggtt ttctttgaag gctctgtagc ccgatttcac tgccaagacq 420
gattcaagct gaagggcgct acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480
qctqqatccc aaqtqataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaatcg 540
aagatgctga gattcataac aagacatata gacatggaga gaagctaatc atcacttgtc 600
atgaaggatt caagatccgg taccccgacc tacacaatat ggtttcatta tgtcgcgatg 660
atggaacgtg gaataatctg cocatctgtc aaggetgeet gagaceteta geetetteta 720
atggctatgt aaacatctct gagctccaga cctccttccc ggtggggact gtgatctcct 780
ateqctqctt teceggattt aaacttgatg ggtetgegta tettgagtge ttacaaaacc 840
ttatctggtc gtccagccca ccccggtgcc ttgctctgga agcccaagtc tgtccactac 900
ctccaatggt gagtcacgga gatttcgtct gccacccgcg gccttgtgag cgctacaacc 960
acggaactgt ggtggagttt tactgcgatc ctggctacag cctcaccagc gactacaagt 1020
acatcacctg ccagtatgga gagtggtttc cttcttatca agtctactgc atcaaatcag 1080
agcaaacqtg gcccagcacc catgagaccc tcctgaccac gtggaagatt gtggcgttca 1140
```

```
eggeaaceag tgtgetgetg gtgetgetge tegteateet ggeeaggatg tteeagacea 1200
agttcaagge ccaettteee eccaggggge eteceeggag tteeageagt gaeeetgaet 1260
ttqtqqtqqt aqacqqcqtq cccqtcatqc tcccqtccta tqacqaaqct qtgagtggcg 1320
qcttqagtqc cttaggcccc gggtacatgg cctctgtggg ccagggctgc cccttacccg 1380
tqqacqacca qaqccccca qcataccccg gctcagggga cacggacaca ggcccagggg 1440
aqtcaqaaac ctgtqacaqc qtctcaqqct cttctgagct gctccaaagt ctgtattcac 1500
ctcccaggtg ccaagagagc acccaccetg cttcggacaa ccctgacata attgccagca 1560
cggcagagga ggtggcatcc accagcccag gcatccatca tgcccactgg gtgttgttcc 1620
taagaaactg attgattaaa aaatttccca aagtgtcctg aagtgtctct tcaaatacat 1680
gttgatctgt ggagttgatt cctttccttc tcttggtttt agacaaatgt aaacaaagct 1740
ctgatcctta aaattgctat gctgatagag tggtgagggc tggaagcttg atcaagtcct 1800
gtttcttctt gacacagact gattaaaaaat taaaagnaaa aaa
<210> 132
<211> 490
<212> PRT
<213> Homo sapiens
<400> 132
Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln
                  5
                                     10
                                                          15
Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val
             20
                                 25
Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr
                             40
Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu
Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val
                                          75
Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys
                 85
                                     90
Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser
                                105
Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu
                            120
Asp Ala Glu Ile His Asn Lys Thr Tyr Arq His Gly Glu Lys Leu Ile
    130
                        135
Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn
                    150
                                         155
Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile
                                                         175
                165
                                    170
Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn
```

			180					185					190		
Ile	Ser	Glu 195	Leu	Gln	Thr	Ser	Phe 200	Pro	Val	Gly	Thr	Val 205	Ile	Ser	Tyr
Arg	Cys 210	Phe	Pro	Gly	Phe	Lys 215	Leu	Asp	Gly	Ser	Ala 220	Tyr	Leu	Glu	Сув
Leu 225	Gln	Asn	Leu	Ile	Trp 230	Ser	Ser	Ser	Pro	Pro 235	Arg	Cys	Leu	Ala	Leu 240
Glu	Ala	Gln	Val	Cys 245	Pro	Leu	Pro	Pro	Met 250	Val	Ser	His	Gly	Asp 255	Phe
Val	Cys	His	Pro 260	Arg	Pro	Cys	Glu	Arg 265	Tyr	Asn	His	Gly	Thr 270	Val	Val
Glu	Phe	Tyr 275	Cys	Asp	Pro	Gly	Tyr 280	Ser	Leu	Thr	Ser	Asp 285	Tyr	Lys	Tyr
Ile	Thr 290	Cys	Gln	Tyr	Gly	Glu 295	Trp	Phe	Pro	Ser	Tyr 300	Gln	Val	Tyr	Cys
Ile 305	Lys	Ser	Glu	Gln	Thr 310	Trp	Pro	Ser	Thr	His 315	Glu	Thr	Leu	Leu	Thr 320
Thr	Trp	Lys	Ile	Val 325	Ala	Phe	Thr	Ala	Thr 330	Ser	Val	Leu	Leu	Val 335	Leu
Leu	Leu	Val	Ile 340	Leu	Ala	Arg	Met	Phe 345	Gln	Thr	Lys	Phe	Lys 350	Ala	His
Phe	Pro	Pro 355	Arg	Gly	Pro	Pro	Arg 360	Ser	Ser	Ser	Ser	Asp 365	Pro	Asp	Phe
Val	Val 370	Val	Asp	Gly	Val	Pro 375	Val	Met	Leu	Pro	Ser 380	Tyr	Asp	Glu	Ala
Val 385	Ser	Gly	Gly	Leu	Ser 390	Ala	Leu	Gly	Pro	Gly 395	Tyr	Met	Ala	Ser	Val 400
Gly	Gln	Gly	Cys	Pro 405	Leu	Pro	Val	Asp	Asp 410	Gln	Ser	Pro	Pro	Ala 415	Tyr
Pro	Gly	Ser	Gly 420	Asp	Thr	Asp	Thr	Gly 425	Pro	Gly	Glu	Ser	Glu 430	Thr	Cys
Asp	Ser	Val 435	Ser	Gly	Ser	Ser	Glu 440	Leu	Leu	Gln	Ser	Leu 445	Tyr	Ser	Pro
Pro	Arg	Cys	Gln	Glu	Ser	Thr	His	Pro	Ala	Ser	Asp	Asn	Pro	Asp	Ile

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His465470475480	
His Ala His Trp Val Leu Phe Leu Arg Asn 485 490	
<210> 133 <211> 23 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 133 atctcctatc gctgctttcc cgg	23
<210> 134 <211> 23 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 134 agccaggatc gcagtaaaac tcc	23
<210> 135 <211> 50 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 135 atttaaactt gatgggtctg cgtatcttga gtgcttacaa aaccttatct	50
<210> 136 <211> 1815 <212> DNA <213> Homo sapiens	
<pre><400> 136 cccacgcgtc cgctccgcgc cctcccccc gcctcccgtg cggtccgtcg gtggcctaga gatgctgctg ccgcggttgc agttgtcgcg cacgcctctg cccgcagcc cgctccaccg ccgtagcgcc cgagtgtcgg ggggcgcacc cgagtcgggc catgaggccg ggaaccgcgc tacaggccgt gctgctggc gtgctgctgg tggggctgcg ggccgcgacg ggtcgctgc tgagtgcctc ggatttggac ctcagaggag ggcagccagt ctgccgggga gggacacaga</pre>	120 180 240

```
qqccttqtta taaaqtcatt tacttccatg atacttctcg aagactgaac tttgaggaag 360
ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtct gaagatgaac 420
aqaaactqat aqaaaaqttc attqaaaacc tcttgccatc tgatggtgac ttctggattg 480
ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540
ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tcctgcggca 600
gcgaggtctg cgtggtcatg taccatcagc catcggcacc cgctggcatc ggaggcccct 660
acatgttcca gtggaatgat gaccggtgca acatgaagaa caatttcatt tgcaaatatt 720
ctgatgagaa accagcagtt ccttctagag aagctgaagg tgaggaaaca gagctgacaa 780
cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaagta 840
gagaagetge cttgaatetg geetacatee taateeceag catteceett eteeteetee 900
ttgtggtcac cacagttgta tgttgggttt ggatctgtag aaaaagaaaa cgggagcagc 960
cagaccctag cacaaagaag caacacacca tctggccctc tcctcaccag ggaaacagcc 1020
cggacctaga ggtctacaat gtcataagaa aacaaagcga agctgactta gctgagaccc 1080
ggccagacct gaagaatatt tcattccgag tgtgttcggg agaagccact cccgatgaca 1140
tgtcttgtga ctatgacaac atggctgtga acccatcaga aagtgggttt gtgactctgg 1200
tqaqcqtqqa qaqtqqattt qtqaccaatq acatttatga gttctcccca gaccaaatgg 1260
qqaqqaqtaa qqaqtctqqa tqqqtqqaaa atqaaatata tggttattag gacatataaa 1320
aaactgaaac tgacaacaat ggaaaagaaa tgataagcaa aatcctctta ttttctataa 1380
ggaaaataca cagaaggtct atgaacaagc ttagatcagg tcctgtggat gagcatgtgg 1440
tececacqae etectqttqq acceccacqt tttqqctqta teetttatee cagecagtea 1500
tccagctcga ccttatgaga aggtaccttg cccaggtctg gcacatagta gagtctcaat 1560
aaatgtcact tggttggttg tatctaactt ttaagggaca gagctttacc tggcagtgat 1620
aaagatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acagcagcac 1680
atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740
ttqqcctqtq catcqqcaat tctcatatct gtttttttca aagaataaaa tcaaataaag 1800
agcaggaaaa aaaaa
<210> 137
<211> 382
<212> PRT
<213> Homo sapiens
<400> 137
Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu
Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu
                                 25
             2.0
Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro
         35
Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe
Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gln Leu Val Ser
                                         75
 65
                     70
Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn
Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu
                                105
            100
```

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr 115 120 125

Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser 130 135 140

Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro 145 150 155 160

Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys 165 170 175

Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala 180 185 190

Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro 195 200 205

Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys 210 215 220

Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser 225 230 235 240

Ile Pro Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val 245 250 255

Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys 260 265 270

Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp 275 280 285

Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala 290 295 300

Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly 305 310 315 320

Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val 325 330 335

Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly
340 345 350

Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg 355 360 365

Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr 370 375 380

<210> 138

```
<211> 50
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 138
gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca
                                                                   50
<210> 139
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 139
                                                                   24
aagccaaaga agcctgcagg aggg
<210> 140
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 140
                                                                   24
cagtccaagc ataaaggtcc tggc
<210> 141
<211> 1514
<212> DNA
<213> Homo sapiens
<400> 141
ggggtetece teagggeegg gaggeaeage ggteeetget tgetgaaggg etggatgtae 60
gcatccgcag gttcccgcgg acttgggggc gcccgctgag ccccggcgcc cgcagaagac 120
ttgtgtttgc ctcctgcagc ctcaacccgg agggcagcga gggcctacca ccatgatcac 180
tggtgtgttc agcatgcgct tgtggacccc agtgggcgtc ctgacctcgc tggcgtactg 240
cctgcaccag cggcggtgg ccctggccga gctgcaggag gccgatggcc agtgtccggt 300
cgaccgcagc ctgctgaagt tgaaaatggt gcaggtcgtg tttcgacacg gggctcggag 360
tecteteaaq eeqeteeege tqqaqqaqea gqtaqaqtqq aacceeeage tattaqaggt 420
cccaccccaa actcagtttg attacacagt caccaatcta gctggtggtc cgaaaccata 480
ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540
gctgaccaag gtgggcatgc agcaaatgtt tgccttggga gagagactga ggaagaacta 600
tgtggaagac attccctttc tttcaccaac cttcaaccca caggaggtct ttattcgttc 660
cactaacatt tttcggaatc tggagtccac ccgttgtttg ctggctgggc ttttccagtg 720
```

```
tcaqaaaqaa qqacccatca tcatccacac tgatgaagca gattcagaag tcttgtatcc 780
caactaccaa aqctqctqqa qcctqaqqca qaqaaccaga ggccggaqgc agactgcctc 840
tttacageca ggaateteag aggatttgaa aaaggtgaag gacaggatgg gcattgacag 900
tagtgataaa gtggacttct tcatcctcct ggacaacgtg gctgccgagc aggcacacaa 960
cctcccaagc tgccccatgc tgaagagatt tgcacggatg atcgaacaga gagctgtgga 1020
cacatcettg tacatactge ceaaggaaga cagggaaagt etteagatgg cagtaggeee 1080
attectecae atectagaga geaacetget gaaageeatg gaetetgeea etgeeeeega 1140
caagatcaga aagctgtatc tctatgcggc tcatgatgtg accttcatac cgctcttaat 1200
gaccetgggg atttttgace acaatggce accetttget gttgacetga ccatggaact 1260
ttaccagcac ctggaatcta aggagtggtt tgtgcagctc tattaccacg ggaaggagca 1320
ggtgccgaga ggttgccctg atgggctctg cccgctggac atgttcttga atgccatgtc 1380
agtttatacc ttaagcccag aaaaatacca tgcactctgc tctcaaactc aggtgatgga 1440
agttggaaat gaagagtaac tgatttataa aagcaggatg tgttgatttt aaaataaagt 1500
gcctttatac aatg
<210> 142
<211> 428
<212> PRT
<213> Homo sapiens
<400> 142
Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
             20
                                 25
Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
                 85
                                     90
Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu
            100
                                105
Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly
                            120
Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val
    130
                        135
Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
145
                    150
                                        155
Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu
```

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His 180 185 190

Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys 195 200 205

Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu 210 215 220

Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly 225 230 235 235

Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val 245 250 255

Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg 260 265 270

Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile 275 280 285

Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe 290 295 300

Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr 305 310 315 320

Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val 325 330 335

Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp 340 345 350

Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu 355 360 365

Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val 370 375 380

Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn 385 390 395 400

Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys 405 410 415

Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu
420 425

<210> 143

<211> 24

<212> DNA

<213> Artificial Sequence

_,	20>	
	23> Description of Artificial Sequence: Synthetic oligonucleotide probe	
	00> 143 aactacca aagctgctgg agcc	24
	10> 144 11> 24	
-	12> DNA 13> Artificial Sequence	
	20> 23> Description of Artificial Sequence: Synthetic oligonucleotide probe	
	00> 144 agctctat taccacggga agga	24
<: <:	10> 145 11> 24 12> DNA 13> Artificial Sequence	
	20> 23> Description of Artificial Sequence: Synthetic oligonucleotide probe	
	00> 145 cttcccgt ggtaatagag ctgc	24
<: <:	10> 146 11> 45 12> DNA 13> Artificial Sequence	
	20>	
<:	23> Description of Artificial Sequence: Synthetic oligonucleotide probe	
	00> 146 cagagaac cagaggccgg aggagactgc ctctttacag ccagg	45
<: <:	10> 147 11> 1686 12> DNA 13> Homo sapiens	
	00> 147	
G.	cctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttctag taaatttc agctcatcac cttcacctgc cttggtcatg gctctgctat tctccttga ttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctggtgg	t 120

```
gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt ggggcaccgt 240
gtgtgatgac ggctgggaca ttaaggacgt ggctgtgttg tgccgggagc tgggctgtgg 300
agctgccagc ggaaccccta gtggtatttt gtatgagcca ccagcagaaa aagagcaaaa 360
ggtcctcatc caatcagtca gttgcacagg aacagaagat acattggctc agtgtgagca 420
agaagaagtt tatgattgtt cacatgatga agatgctggg gcatcgtgtg agaacccaga 480
qaqctctttc tecccaqtec caqaqqqtqt caggetggct gacggccctg ggcattgcaa 540
qqqacqcgtg gaagtgaagc accagaacca gtggtatacc gtgtgccaga caggctggag 600
cctccgggcc gcaaaggtgg tgtgccggca gctgggatgt gggagggctg tactgactca 660
aaaacgctgc aacaagcatg cctatggccg aaaacccatc tggctgagcc agatgtcatg 720
ctcaggacga gaagcaaccc ttcaggattg cccttctggg ccttggggga agaacacctg 780
caaccatgat gaagacacgt gggtcgaatg tgaagatccc tttgacttga gactagtagg 840
aggagacaac ctctgctctg ggcgactgga ggtgctgcac aagggcgtat ggggctctgt 900
ctgtgatgac aactggggag aaaaggagga ccaggtggta tgcaagcaac tgggctgtgg 960
gaagtccctc tctccctcct tcagagaccg gaaatgctat ggccctgggg ttggccgcat 1020
ctggctggat aatgttcgtt gctcagggga ggagcagtcc ctggagcagt gccagcacag 1080
attttggggg tttcacgact gcacccacca ggaagatgtg gctgtcatct gctcagtgta 1140
ggtgggcatc atctaatctg ttgagtgcct gaatagaaga aaaacacaga agaagggagc 1200
atttactgtc tacatgactg catgggatga acactgatct tcttctgccc ttggactggg 1260
acttatactt ggtgcccctg attctcaggc cttcagagtt ggatcagaac ttacaacatc 1320
aggtctagtt ctcaggccat cagacatagt ttggaactac atcaccacct ttcctatgtc 1380
tccacattgc acacagcaga ttcccagcct ccataattgt gtgtatcaac tacttaaata 1440
catteteaca cacacaca cacacaca cacacaca cacacataca ccattegtee 1500
tgtttctctg aagaactctg acaaaataca gattttggta ctgaaagaga ttctagagga 1560
acggaatttt aaggataaat tttctgaatt ggttatgggg tttctgaaat tggctctata 1620
atctaattag atataaaatt ctggtaactt tatttacaat aataaagata gcactatgtg 1680
                                                                  1686
ttcaaa
<210> 148
<211> 347
<212> PRT
<213> Homo sapiens
<400> 148
Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly
Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg
                                 25
Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val
                             40
Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu
                         55
Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
 65
Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys
                 85
```

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Val Tyr
100 105 110

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu 115 120 125

Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro 130 135 140

Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr 145 150 155 160

Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys 165 170 175

Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn 180 185 190

Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys 195 200 205

Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly 210 215 220

Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp 225 230 235 240

Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg
245 250 255

Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn 260 265 270

Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly 275 280 285

Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly 290 295 300

Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln 305 310 315 320

Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr 325 330 335

His Gln Glu Asp Val Ala Val Ile Cys Ser Val 340 345

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

agggccaggg cagagaagca gcactcttag gcttgcttac tctacaaggg acagttgcat 1140 ttgttgagac tttaatggag atttgtctca caagtgggaa agactgaaga aacacatctc 1200 gtgcagatct gctggcagag gacaatcaaa aacgacaaca agcttcttcc cagggtgagg 1260 ggaaacactt aaggaataaa tatggagctg gggtttaaca ctaaaaacta gaaataaaca 1320 tctcaaacag taaaaaaaa aaaaaagggc ggccgcgact ctagagtcga cctgcagaag 1380 cttggccgcc atggcccaac ttgtttattg cagcttataa tggttac 1427

<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
1 5 10 15

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
20 25 30

Ala Tyr Leu Arg Asn Ala Val Val Ile Thr Gly Ala Thr Ser Gly
35 40 45

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu 50 55 60

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu 65 70 75 80

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu 85 90 95

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala 100 105 110

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala 115 120 125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp 130 135 140

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys 145 150 155 160

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala 165 170 175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr 180 185 190

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala 195 200 205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

	210					215					220					
Ile 225	His	Thr	Asn	Leu	Ser 230	Val	Asn	Ala	Ile	Thr 235	Ala	Asp	Gly	Ser	Arg 240	
Tyr	Gly	Val	Met	Asp 245	Thr	Thr	Thr	Ala	Gln 250	Gly	Arg	Ser	Pro	Val 255	Glu	
Val	Ala	Gln	Asp 260	Val	Leu	Ala	Ala	Val 265	Gly	Lys	Lys	Lys	Lys 270	Asp	Val	
Ile	Leu	Ala 275	Asp	Leu	Leu	Pro	Ser 280	Leu	Ala	Val	Tyr	Leu 285	Arg	Thr	Leu	
Ala	Pro 290	Gly	Leu	Phe	Phe	Ser 295	Leu	Met	Ala	Ser	Arg 300	Ala	Arg	Lys	Glu	
Arg 305	Lys	Ser	Lys	Asn	Ser 310											
<211)> 19 L> 24	1														
	2 > Di 3 > Ai		icia	l Se	quen	ce										
<220 <223	3 > De		iptio nucle				cial	Seqi	uence	e: S	ynth	etic				
)> 19 gctaa		tggt	gete	tg t	ggc										24
)> 1!															
	L> 20 2> DI															
<213	3 > A	rtif	icia	l Se	quen	ce										
<220 <223	3 > De		iptio nucle				cial	Seq	uenc	e: S	ynth	etic				
)> 1! ggcaa		tgag	catt	cc											20
)> 1!															
	l> 24 2> DI															
			icia	l Se	quen	ce										
<220																
<223			iptio					Seq	uenc	e: S	ynth	etic				

```
<400> 156
                                                                24
tcatactgtt ccatctcggc acgc
<210> 157
<211> 50
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
     oligonucleotide probe
<400> 157
                                                                50
aatggtgggg ccctagaaga gctcatcaga gaactcaccg cttctcatgc
<210> 158
<211> 1771
<212> DNA
<213> Homo sapiens
<400> 158
cccacqcqtc cqctqqtqtt aqatcqaqca accctctaaa agcagtttag agtggtaaaa 60
aaaaaaaaa acacaccaaa cgctcgcagc cacaaaaggg atgaaatttc ttctggacat 120
cetectqett eteceqttae tqateqtetq etecetagag teettegtga agetttttat 180
tcctaagagg agaaaatcag tcaccggcga aatcgtgctg attacaggag ctgggcatgg 240
aattqqqaqa ctqactqcct atqaatttgc taaacttaaa agcaagctgg ttctctggga 300
tataaataag catggactgg aggaaacagc tgccaaatgc aagggactgg gtgccaaggt 360
tcataccttt qtqqtaqact qcagcaaccg agaagatatt tacagctctg caaagaaggt 420
gaaggcagaa attggagatg ttagtatttt agtaaataat gctggtgtag tctatacatc 480
agatttgttt gctacacaag atcctcagat tgaaaagact tttgaagtta atgtacttgc 540
acatttctgg actacaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600
tqtcactqtq gcttcqqcaq ctggacatqt ctcggtcccc ttcttactqq cttactqttc 660
aagcaagttt gctgctgttg gatttcataa aactttgaca gatgaactgg ctgccttaca 720
aataactgga gtcaaaacaa catgtctgtg tcctaatttc gtaaacactg gcttcatcaa 780
aaatccaagt acaagtttgg gacccactct ggaacctgag gaagtggtaa acaggctgat 840
gcatgggatt ctgactgagc agaagatgat ttttattcca tcttctatag cttttttaac 900
aacattggaa aggatccttc ctgagcgttt cctggcagtt ttaaaacgaa aaatcagtgt 960
taagtttgat gcagttattg gatataaaat gaaagcgcaa taagcaccta gttttctgaa 1020
aactgattta ccaggtttag gttgatgtca tctaatagtg ccagaatttt aatgtttgaa 1080
cttctgtttt ttctaattat ccccatttct tcaatatcat ttttgaggct ttggcagtct 1140
tcatttacta ccacttgttc tttagccaaa agctgattac atatgatata aacagagaaa 1200
tacctttaga ggtgacttta aggaaaatga agaaaaagaa ccaaaatgac tttattaaaa 1260
taatttccaa gattatttgt ggctcacctg aaggctttgc aaaatttgta ccataaccgt 1320
ttatttaaca tatattttta tttttqattq cacttaaatt ttgtataatt tgtgtttctt 1380
tttctqttct acataaaatc aqaaacttca aqctctctaa ataaaatgaa ggactatatc 1440
tagtggtatt tcacaatgaa tatcatgaac tctcaatggg taggtttcat cctacccatt 1500
qccactctgt ttcctgagag atacctcaca ttccaatgcc aaacatttct gcacagggaa 1560
gctagaggtg gatacacgtg ttgcaagtat aaaagcatca ctgggattta aggagaattg 1620
aqaqaatqta cccacaaatq gcagcaataa taaatggatc acacttaaaa aaaaaaaaa 1680
1771
aaaaaaaaa aaaaaaaaa aaaaaaaaa a
```

<211> 300

<212> PRT

<213> Homo sapiens

<400> 159

Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Pro Leu Leu Ile Val 1 5 10 15

Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg Arg Lys
20 25 30

Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile 35 40 45

Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val
50 55 60

Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys 65 70 75 80

Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn 85 90 95

Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly
100 105 110

Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp 115 120 125

Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn 130 135 140

Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Thr 145 150 155 160

Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His 165 170 175

Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala 180 185 190

Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile 195 200 205

Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly 210 215 220

Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu 225 230 235 240

Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met 245 250 255

Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile 260 265 270	
Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys 275 280 285	
Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln 290 295 300	
<210> 160 <211> 23 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 160 ggtgaaggca gaaattggag atg 23	3
<210> 161 <211> 24 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 161 atcccatgca tcagcctgtt tacc 24	Ŀ
<210> 162 <211> 48 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 162 gctggtgtag tctatacatc agatttgttt gctacacaag atcctcag 48	3
<210> 163 <211> 2076 <212> DNA <213> Homo sapiens	
<400> 163 cccacgcgtc cgcggacgcg tgggtcgact agttctagat cgcgagcggc cgcccgcggc 60 tcagggagga gcaccgactg cgccgcaccc tgagagatgg ttggtgccat gtggaaggtg 12	

```
attqtttcgc tqgtcctgtt gatgcctggc ccctgtgatg ggctgtttcg ctccctatac 180
agaagtgttt ccatgccacc taagggagac tcaggacagc cattatttct caccccttac 240
attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggtcggccc tttcccagga 300
ctgaacatga agagttatgc cggcttcctc accgtgaata agacttacaa cagcaacctc 360
ttcttctqqt tcttcccaqc tcaqatacaq ccaqaaqatq ccccaqtaqt tctctggcta 420
cagggtgggc cgggaggttc atccatgttt ggactctttg tggaacatgg gccttatgtt 480
gtcacaagta acatgacctt gcgtgacaga gacttcccct ggaccacaac gctctccatg 540
ctttacattg acaatccagt gggcacaggc ttcagtttta ctgatgatac ccacggatat 600
gcagtcaatg aggacgatgt agcacgggat ttatacagtg cactaattca gtttttccag 660
atatttcctg aatataaaaa taatgacttt tatgtcactg gggagtctta tgcagggaaa 720
tatqtqccaq ccattqcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780
aacctgaacg gaattgctat tggagatgga tattctgatc ccgaatcaat tatagggggc 840
tatgcagaat tcctgtacca aattggcttg ttggatgaga agcaaaaaaa gtacttccag 900
aagcagtgcc atgaatgcat agaacacatc aggaagcaga actggtttga ggcctttgaa 960
atactggata aactactaga tggcgactta acaagtgatc cttcttactt ccagaatgtt 1020
acaggatgta gtaattacta taactttttg cggtgcacgg aacctgagga tcagctttac 1080
tatgtgaaat ttttgtcact cccagaggtg agacaagcca tccacgtggg gaatcagact 1140
tttaatgatg gaactatagt tgaaaagtac ttgcgagaag atacagtaca gtcagttaag 1200
ccatggttaa ctgaaatcat gaataattat aaggttctga tctacaatgg ccaactggac 1260
atcatcgtgg cagctgccct gacagagcgc tccttgatgg gcatggactg gaaaggatcc 1320
caggaataca agaaggcaga aaaaaaagtt tggaagatct ttaaatctga cagtgaagtg 1380
qctqqttaca tccqqcaagc qqqtgacttc catcaggtaa ttattcgagg tggaggacat 1440
attttaccct atgaccagcc tctgagagct tttgacatga ttaatcgatt catttatgga 1500
aaaggatggg atccttatgt tggataaact accttcccaa aagagaacat cagaggtttt 1560
cattgctgaa aagaaaatcg taaaaacaga aaatgtcata ggaataaaaa aattatcttt 1620
tcatatctgc aagatttttt tcatcaataa aaattatcct tgaaacaagt gagcttttgt 1680
ttttgggggg agatgtttac tacaaaatta acatgagtac atgagtaaga attacattat 1740
ttaacttaaa ggatgaaagg tatggatgat gtgacactga gacaagatgt ataaatgaaa 1800
ttttagggtc ttgaatagga agttttaatt tcttctaaga gtaagtgaaa agtgcagttg 1860
taacaaacaa aqctqtaaca tctttttctq ccaataacag aagtttggca tgccgtgaag 1920
qtqtttqqaa atattattqq ataaqaataq ctcaattatc ccaaataaat ggatgaagct 1980
ataatagttt tggggaaaag attctcaaat gtataaagtc ttagaacaaa agaattcttt 2040
gaaataaaaa tattatatat aaaagtaaaa aaaaaa
<210> 164
<211> 476
<212> PRT
<213> Homo sapiens
<400> 164
```

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
1 5 10 15

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser 20 25 30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
35 40 45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

65					70					75					80
Asn	Lys	Thr	Tyr	Asn 85	Ser	Asn	Leu	Phe	Phe 90	Trp	Phe	Phe	Pro	Ala 95	Gln
Ile	Gln	Pro	Glu 100	Asp	Ala	Pro	Val	Val 105	Leu	Trp	Leu	Gln	Gly 110	Gly	Pro
Gly	Gly	Ser 115	Ser	Met	Phe	Gly	Leu 120	Phe	Val	Glu	His	Gly 125	Pro	Tyr	Val
Val	Thr 130	Ser	Asn	Met	Thr	Leu 135	Arg	Asp	Arg	Asp	Phe 140	Pro	Trp	Thr	Thr
Thr 145	Leu	Ser	Met	Leu	Tyr 150	Ile	Asp	Asn	Pro	Val 155	Gly	Thr	Gly	Phe	Ser 160
Phe	Thr	Asp	Asp	Thr 165	His	Gly	Tyr	Ala	Val 170	Asn	Glu	Asp	Asp	Val 175	Ala
Arg	Asp	Leu	Tyr 180	Ser	Ala	Leu	Ile	Gln 185	Phe	Phe	Gln	Ile	Phe 190	Pro	Glu
Tyr	Lys	Asn 195	Asn	Asp	Phe	Tyr	Val 200	Thr	Gly	Glu	Ser	Tyr 205	Ala	Gly	Lys
Tyr	Val 210	Pro	Ala	Ile	Ala	His 215	Leu	Ile	His	Ser	Leu 220	Asn	Pro	Val	Arg
Glu 225	Val	Lys	Ile	Asn	Leu 230	Asn	Gly	Ile	Ala	Ile 235	Gly	Asp	Gly	Tyr	Ser 240
Asp	Pro	Glu	Ser	Ile 245	Ile	Gly	Gly	Tyr	Ala 250	Glu	Phe	Leu	Tyr	Gln 255	Ile
Gly	Leu	Leu	Asp 260	Glu	Lys	Gln	Lys	Lys 265	Tyr	Phe	Gln	Lys	Gln 270	Cys	His
Glu	Cys	Ile 275	Glu	His	Ile	Arg	_			Trp		Glu 285	Ala	Phe	Glu
Ile	Leu 290	Asp	Lys	Leu	Leu	Asp 295	Gly	Asp	Leu	Thr	Ser 300	Asp	Pro	Ser	Tyr
Phe 305	Gln	Asn	Val	Thr	Gly 310	Cys	Ser	Asn	Tyr	Tyr 315	Asn	Phe	Leu	Arg	Cys 320
Thr	Glu	Pro	Glu	Asp 325	Gln	Leu	Tyr	Tyr	Val 330	Lys	Phe	Leu	Ser	Leu 335	Pro
Glu	Val	Arg	Gln 340	Ala	Ile	His	Val	Gly 345	Asn	Gln	Thr	Phe	Asn 350	Asp	Gly

Thr	Ile	Val 355	Glu	Lys	Tyr	Leu	Arg 360	Glu	Asp	Thr	Val	Gln 365	Ser	Val	Lys	
Pro	Trp 370	Leu	Thr	Glu	Ile	Met 375	Asņ	Asn	Tyr	Lys	Val 380	Leu	Ile	Tyr	Asn	
Gly 385	Gln	Leu	Asp	Ile	Ile 390	Val	Ala	Ala	Ala	Leu 395	Thr	Glu	Arg	Ser	Leu 400	
Met	Gly	Met	Asp	Trp 405	Lys	Gly	Ser	Gln	Glu 410	Tyr	Lys	Lys	Ala	Glu 415	Lys	
Lys	Val	Trp	Lys 420	Ile	Phe	Lys	Ser	Asp 425	Ser	Glu	Val	Ala	Gly 430	Tyr	Ile	
Arg	Gln	Ala 435	Gly	Asp	Phe	His	Gln 440	Val	Ile	Ile	Arg	Gly 445	Gly	Gly	His	
Ile	Leu 450	Pro	Tyr	Asp	Gln	Pro 455	Leu	Arg	Ala	Phe	Asp 460	Met	Ile	Asn	Arg	
Phe 465	Ile	Tyr	Gly	Lys	Gly 470	Trp	Asp	Pro	Tyr	Val 475	Gly					
<211 <212	0> 16 L> 24 2> DI B> A	1 NA	icia	l Sed	quen	ce										
<220 <223	3> De		-		f Art		cial	Seq	uence	e: S	ynth	etic				
)> 10 catgo		ccta	aggga	ag a	ctc										24
<211 <212)> 16 L> 24 2> DI B> A	1 NA	icia	l Sed	quen	ce										
<220 <223	3> De				f Art		cial	Seq	uence	e: S	ynth	etic				
)> 10		atac:	aatoo	gc t	aac										24
			9090	.u.c.	5 0 0	22~										
)> 10 L> 24	-					,									
	2> DI															
			icia	l Se	quen	ce										

```
<220>
<223> Description of Artificial Sequence: Synthetic
     oligonucleotide probe
<400> 167
                                                                24
ageteteaga ggetggteat aggg
<210> 168
<211> 50
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 168
                                                                50
gtcggccctt tcccaggact gaacatgaag agttatgccg gcttcctcac
<210> 169
<211> 2477
<212> DNA
<213> Homo sapiens
<400> 169
cgagggcttt tccggctccg gaatggcaca tgtgggaatc ccagtcttgt tggctacaac 60
attittccct ttcctaacaa gttctaacag ctgttctaac agctagtgat caggggttct 120
tcttgctgga gaagaaaggg ctgagggcag agcagggcac tctcactcag ggtgaccagc 180
teettgeete tetgtggata acagageatg agaaagtgaa gagatgeage ggagtgaggt 240
gatggaagtc taaaatagga aggaattttg tgtgcaatat cagactctgg gagcagttga 300
cctggagagc ctgggggagg gcctgcctaa caagctttca aaaaacagga gcgacttcca 360
ctgggctggg ataagacgtg ccggtaggat agggaagact gggtttagtc ctaatatcaa 420
attgactggc tgggtgaact tcaacagcct tttaacctct ctgggagatg aaaacgatgg 480
tatagcataa aggctagaga ccaaaataga taacaggatt ccctgaacat tcctaagagg 600
gaqaaagtat gttaaaaata gaaaaaccaa aatgcagaag gaggagactc acagagctaa 660
accaggatgg ggaccetggg teaggeeage etetttgete eteceggaaa ttatttttgg 720
tctgaccact ctgccttgtg ttttgcagaa tcatgtgagg gccaaccggg gaaggtggag 780
caqatgaqca cacacaggag ccgtctcctc accgccgccc ctctcagcat ggaacagagg 840
caqccctggc cccgggccct ggaggtggac agccgctctg tggtcctgct ctcagtggtc 900
tgggtgctgc tggcccccc agcagccggc atgcctcagt tcagcacctt ccactctgag 960
aatcgtgact ggaccttcaa ccacttgacc gtccaccaag ggacgggggc cgtctatgtg 1020
ggggccatca accgggtcta taagctgaca ggcaacctga ccatccaggt ggctcataag 1080
acagggccag aagaggacaa caagtctcgt tacccgcccc tcatcgtgca gccctgcagc 1140
gaagtgctca ccctcaccaa caatgtcaac aagctgctca tcattgacta ctctgagaac 1200
cgcctgctgg cctgtgggag cctctaccag ggggtctgca agctgctgcg gctggatgac 1260
ctcttcatcc tggtggagcc atcccacaag aaggagcact acctgtccag tgtcaacaag 1320
acgggcacca tgtacggggt gattgtgcgc tctgagggtg aggatggcaa gctcttcatc 1380
qqcacqqctq tqqatqqqaa gcaggattac ttcccgaccc tgtccagccg gaagctgccc 1440
cgagaccctg agtcctcagc catgctcgac tatgagctac acagcgattt tgtctcctct 1500
ctcatcaaga tcccttcaga caccttggcc ctggtctccc actttgacat cttctacatc 1560
tacggctttg ctagtggggg ctttgtctac tttctcactg tccagcccga gacccctgag 1620
ggtgtggcca tcaactccgc tggagacctc ttctacacct cacgcatcgt gcggctetgc 1680
```



```
aaggatgace ccaagtteca cteatacgtg teeetgeet teggetgeae cegggeeggg 1740 gtggaatace geeteetgea ggetgettae etggeeaage etggggaete aetggeeaag 1860 cagtateaee aecegeega tgaetetgee etgtgtgeet teeetateeg ggeeateaae 1920 ttgeagatea aggaegeet geagteetge taecagggeg agggeaacet ggageteaae 1980 tggetgetgg ggaaggaegt eeagteetge taecagggeg agggeaacet ggageteaae 1980 tgtggaetgg ggaaggaegt eeagteetge taecagggeg agggeaacet ggageteaae 1980 tgtggaetgg acateaaeea geeeetggga ggeteaaete eagtggaggg eetgaeeetg teeeeatega tgataaette 2040 tgtggaetgg acateaaeea geeeetggga ggeteaaete eagtggaggg eetgaeeetg 2100 taeaeeaea geaggaeeg eatgaeetet gtggeeteet aegtttaeaa eggetaeage 2160 gtggtttttg tggggaetaa gagtggeaag etgaaaaagg taagagteta tgagtteaga 2220 tgeteeaatg eeatteaeet eeteageaaa gagteeetet tggaaaggtag etattggtgg 2280 agatttaaet ataggeaaet ttatttett ggggaaeaaa ggtgaaatgg ggaggtaaga 2340 gtaaggaatg eaagegtatt teeaatatte eeaaaettta agaaaaaaet ttaagaaggt 2460 acateetgea aageaaa
```

<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr
1 5 10 15

Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly
20 25 30

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu 35 40 45

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala 50 55 60

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
65 70 75 80

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His
85 90 95

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly
100 105 110

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr 115 120 125

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp 130 135 140

Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val 145 150 155 160

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser 165 170 175 Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys 180 185 190

Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys
195 200 205

Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly 210 215 220

Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr 225 230 235 240

Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys 245 250 255

Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His
260 265 270

Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala 275 280 285

Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly 290 295 300

Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val 305 310 315 320

Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg 325 330 335

Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe 340 345 350

Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr 355 360 365

Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser 370 375 380

Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr 385 390 395 400

His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala 405 410 415

Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu
420 425 430

Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr 435 440 445

Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

4	150					455					460					
Gln I 465	?ro	Leu	Gly	Gly	Ser 470	Thr	Pro	Val	Glu	Gly 475	Leu	Thr	Leu	Tyr	Thr 480	
Thr S	Ser	Arg	Asp	Arg 485	Met	Thr	Ser	Val	Ala 490	Ser	Tyr	Val	Tyr	Asn 495	Gly	
Tyr S	Ser	Val	Val 500	Phe	Val	Gly	Thr	Lys 505	Ser	Gly	Lys	Leu	Lys 510	Lys	Val	
Arg V	/al	Tyr 515	Glu	Phe	Arg	Cys	Ser 520	Asn	Ala	Ile	His	Leu 525	Leu	Ser	Lys	
Glu S	Ser 530	Leu	Leu	Glu	Gly	Ser 535	Tyr	Trp	Trp	Arg	Phe 540	Asn	Tyr	Arg	Gln	
Leu 7 545	Гуr	Phe	Leu	Gly	Glu 550	Gln	Arg									
<210: <211: <212: <213: <220: <223:	> 20 > DN > Ar > De ol	JA tifi escri		on of	- E Art	ific	cial	Sequ	ience	e: Sy	ynthe	etic				
<4003 tggaa			cctcc	etgea	ag	•										20
<210: <211: <212: <213:	> 24 > DN	IA	icial	L Sec	quenc	ce										
<220: <223:	> De		iptic nucle				cial	Seqı	ıence	e: Sy	ynthe	etic				
<400: cttct			tgga	agaag	ga to	ggc										24
<210: <211: <212: <213:	> 43 > DN	IA	icial	l Sec	quenc	ce										
<220: <223:	> De		iptic nucle					Seqi	uence	e: Sy	ynthe	etic				

```
<400> 173
                                                                  42
ggactcactg gcccaggcct tcaatatcac cagccaggac gat
<210> 174
<211> 3106
<212> DNA
<213> Homo sapiens
<220>
<221> modified_base
<222> (1683)
<223> a, t, c or g
<400> 174
aggetecege gegeggetga gtgeggaetg gagtgggaac eegggteeee gegettagag 60
aacacgcgat gaccacgtgg agcctccggc ggaggccggc ccgcacgctg ggactcctgc 120
tgctggtcgt cttgggcttc ctggtgctcc gcaggctgga ctggagcacc ctggtccctc 180
tgcggctccg ccatcgacag ctggggctgc aggccaaggg ctggaacttc atgctggagg 240
attecacett etggatette gggggeteca tecactattt eegtgtgeee agggagtaet 300
ggagggaccg cctgctgaag atgaaggcct gtggcttgaa caccctcacc acctatgttc 360
cgtggaacct gcatgagcca gaaagaggca aatttgactt ctctgggaac ctggacctgg 420
aggeettegt eetgatggee geagagateg ggetgtgggt gattetgegt eeaggeeeet 480
acatetgeag tgagatggae eteggggget tgeecagetg getaeteeaa gaceetggea 540
tgaggctgag gacaacttac aagggcttca ccgaagcagt ggacctttat tttgaccacc 600
tgatgtccag ggtggtgcca ctccagtaca agcgtggggg acctatcatt gccgtgcagg 660
tggagaatga atatggttcc tataataaag accccgcata catgccctac gtcaagaagg 720
cactggagga ccgtggcatt gtggaactgc tcctgacttc agacaacaag gatgggctga 780
gcaaggggat tgtccaggga gtcttggcca ccatcaactt gcagtcaaca cacgagctgc 840
agctactgac cacctttctc ttcaacgtcc aggggactca gcccaagatg gtgatggagt 900
actggacggg gtggtttgac tcgtggggag gccctcacaa tatcttggat tcttctgagg 960
ttttgaaaac cgtgtctgcc attgtggacg ccggctcctc catcaacctc tacatgttcc 1020
acggaggeac caactttggc ttcatgaatg gagccatgca cttccatgac tacaagtcag 1080
atqtcaccaq ctatqactat gatgctgtgc tgacagaagc cggcgattac acggccaagt 1140
acatgaaget tegagaette tteggeteea teteaggeat eceteteeet ececeacetg 1200
accttettee caagatgeeg tatgageeet taaegeeagt ettgtacetg tetetgtggg 1260
acgccctcaa gtacctgggg gagccaatca agtctgaaaa gcccatcaac atggagaacc 1320
tgccagtcaa tgggggaaat ggacagtcct tcgggtacat tctctatgag accagcatca 1380
cctcgtctgg catcctcagt ggccacgtgc atgatcgggg gcaggtgttt gtgaacacag 1440
tatccatagg attcttggac tacaagacaa cgaagattgc tgtccccctg atccagggtt 1500
acaccgtgct gaggatcttg gtggagaatc gtgggcgagt caactatggg gagaatattg 1560
atgaccagcg caaaggetta attggaaate tetatetgaa tgatteacce etgaaaaaet 1620
tcagaatcta tagcctggat atgaagaaga gcttctttca gaggttcggc ctggacaaat 1680
ggngttccct cccagaaaca cccacattac ctgctttctt cttgggtagc ttgtccatca 1740
qctccacqcc ttqtqacacc tttctgaagc tggagggctg ggagaagggg gttgtattca 1800
tcaatggcca gaaccttgga cgttactgga acattggacc ccagaagacg ctttacctcc 1860
caggtecetg gttgageage ggaateaace aggteategt ttttgaggag acgatggegg 1920
gccctgcatt acagttcacg gaaacccccc acctgggcag gaaccagtac attaagtgag 1980
eggtggcacc cectectget ggtgccagtg ggagactgcc geeteetett gacetgaage 2040
etggtggetg etgeeceaec ceteaetgea aaageatete ettaagtage aaceteaggg 2100
actgggggct acagtctgcc cctgtctcag ctcaaaaccc taagcctgca gggaaaggtg 2160
ggatggctct gggcctggct ttgttgatga tggctttcct acagccctgc tcttgtgccg 2220
```

aggetgtegg getgteteta gggtgggage agetaateag ategeeeage etttggeeet 2280

```
caqaaaaagt gctgaaacgt gcccttgcac cggacgtcac agccctgcga gcatctgctg 2340
gactcaggeg tgctctttgc tggttcctgg gaggettggc cacatecete atggeeceat 2400
tttatccccg aaatcctggg tgtgtcacca gtgtagaggg tggggaaggg gtgtctcacc 2460
tqaqctqact ttqttcttcc ttcacaacct tctgagcctt ctttgggatt ctggaaggaa 2520
ctcggcgtga gaaacatgtg acttcccctt tcccttccca ctcgctgctt cccacagggt 2580
qacaqqctqq qctqqaqaaa cagaaatcct caccctgcgt cttcccaagt tagcaggtgt 2640
ctctqqtqtt caqtqaqqaq qacatqtgag tcctggcaga agccatggcc catgtctgca 2700
catccaggga ggaggacaga aggcccagct cacatgtgag tcctggcaga agccatggcc 2760
catqtctqca catccaggga ggaggacaga aggcccagct cacatgtgag tcctggcaga 2820
agccatggcc catgtctgca catccaggga ggaggacaga aggcccagct cacatgtgag 2880
teetqqeaqa agecatggee catgtetgea catecaggga ggaggacaga aggeecaget 2940
cagtggcccc cgctccccac cccccacgcc cgaacagcag gggcagagca gccctccttc 3000
qaaqtqtqtc caaqtccgca tttgagcctt gttctggggc ccagcccaac acctggcttg 3060
qqctcactqt cctgagttgc agtaaagcta taaccttgaa tcacaa
<210> 175
<211> 636
<212> PRT
<213> Homo sapiens
<220>
<221> MOD RES
<222> (539)
<223> Any amino acid
<400> 175
Met Thr Trp Ser Leu Arg Arg Pro Ala Arg Thr Leu Gly Leu
  1
                  5
Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
                         55
     50
Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
                                                    110
            100
                                105
Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
                            120
Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
                                            140
    130
                        135
```

Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu 145 Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro 185 Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp 195 Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile 215 Val Glu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly 225 235 Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu 245 Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro 265 Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly 275 Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala 295 Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly 305 310 315 Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys 325 330 Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly 345 Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile 355 Ser Gly Ile Pro Leu Pro Pro Pro Pro Asp Leu Leu Pro Lys Met Pro Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu 385 390 395 400 Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu 405 Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu

425

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His 440 Asp Arq Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp 455 Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val 475 465 470 Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn 490 Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp 500 505 510 Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser 520 Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr 535 Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr 550 555 545 Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln 590 580 585 Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln 595 Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr 615 Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys 630 625 <210> 176 <211> 2505 <212> DNA <213> Homo sapiens <400> 176 ggggacgcgg agctgagagg ctccgggcta gctaggtgta ggggtggacg ggtcccagga 60 ccctqqtqaq qqttctctac ttggccttcg gtgggggtca agacgcaggc acctacgcca 120 aaqqqqaqca aaqccqqqct cqqcccgagg cccccaggac ctccatctcc caatgttgga 180 qqaatccqac acqtqacqqt ctqtccqccq tctcagacta gaggagcqct gtaaacgcca 240 tggctcccaa gaagctgtcc tgccttcgtt ccctgctgct gccgctcagc ctgacgctac 300

tgctgcccca ggcagacact cggtcgttcg tagtggatag gggtcatgac cggtttctcc 360 tagacqqqqc cccqttccqc tatqtqtctg gcagcctgca ctactttcgg gtaccgcggg 420

```
tgctttgggc cgaccggctt ttgaagatgc gatggagcgg cctcaacgcc atacagtttt 480
atgtgccctg gaactaccac gagccacagc ctggggtcta taactttaat ggcagccggg 540
acctcattgc ctttctgaat gaggcagctc tagcgaacct gttggtcata ctgagaccag 600
qaccttacat ctqtqcaqaq tqqqaqatqq qqqqtctccc atcctqqttq cttcqaaaac 660
ctgaaattca tctaagaacc tcagatccag acttccttgc cgcagtggac tcctggttca 720
aggtettget geccaagata tateeatgge tttateacaa tgggggeaac ateattagea 780
ttcaqqtqqa qaatqaatat qqtaqctaca gagcctgtga cttcagctac atgaggcact 840
tggctgggct cttccgtgca ctgctaggag aaaagatctt gctcttcacc acagatgggc 900
ctgaaggact caagtgtggc teceteeggg gactetatac caetgtagat tttggcccag 960
ctgacaacat gaccaaaatc tttaccctgc ttcggaagta tgaaccccat gggccattgg 1020
taaactetga gtactacaca ggetggetgg attactgggg ccagaatcac tccacacggt 1080
ctgtgtcagc tgtaaccaaa ggactagaga acatgctcaa gttgggagcc agtgtgaaca 1140
tgtacatgtt ccatggaggt accaactttg gatattggaa tggtgccgat aagaagggac 1200
getteettee gattactace agetatgact atgatgeace tatatetgaa geaggggace 1260
ccacacctaa gctttttgct cttcgagatg tcatcagcaa gttccaggaa gttcctttgg 1320
gacetttace tecceegage eccaagatga tgettggace tgtgactetg cacetggttg 1380
ggcatttact ggctttccta gacttgcttt gcccccgtgg gcccattcat tcaatcttgc 1440
caatgacett tgaggetgte aageaggace atggetteat gttgtacega acetatatga 1500
cccataccat ttttgagcca acaccattct gggtgccaaa taatggagtc catgaccgtg 1560
cctatqtgat qqtqqatqqq gtgttccagg gtgttgtgga gcgaaatatg agagacaaac 1620
tatttttgac ggggaaactg gggtccaaac tggatatctt ggtggagaac atggggaggc 1680
tragetttgg gtetaacage agtgaettea agggeetgtt gaagecacea attetgggge 1740
aaacaatcct tacccagtgg atgatgttcc ctctgaaaat tgataacctt gtgaagtggt 1800
ggtttcccct ccagttgcca aaatggccat atcctcaagc tccttctggc cccacattct 1860
actccaaaac atttccaatt ttaggctcag ttggggacac atttctatat ctacctggat 1920
qqaccaaqqq ccaaqtctqq atcaatqqqt ttaacttqqq ccgqtactgq acaaagcagg 1980
qqccacaaca qaccetetac qtqccaaqat teetgetgtt teetagggga geeetcaaca 2040
aaattacatt gctggaacta gaagatgtac ctctccagcc ccaagtccaa tttttggata 2100
agectatect caataqeact aqtaetttqc acaggacaca tateaattcc ettteagetg 2160
atacactqaq tqcctctqaa ccaatqqaqt taagtgggca ctgaaaggta ggccgggcat 2220
ggtggctcat gcctgtaatc ccagcacttt gggaggctga gacgggtgga ttacctgagg 2280
tcaggacttc aagaccagcc tggccaacat ggtgaaaccc cgtctccact aaaaatacaa 2340
aaattagccg ggcgtgatgg tgggcacctc taatcccagc tacttgggag gctgagggca 2400
qqaqaattqc ttqaatccaq qaqqcaqagg ttgcagtgag tggaggttgt accactgcac 2460
tccagcctqq ctqacagtqa gacactccat ctcaaaaaaa aaaaa
                                                                  2505
<210> 177
<211> 654
<212> PRT
<213> Homo sapiens
<400> 177
Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Pro Leu
Ser Leu Thr Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val
```

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala
50 55 60

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr

- Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe 65 70 75 80
- Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe
 85 90 95
- Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala 100 105 110
- Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp 115 120 125
- Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His 130 135 140
- Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe 145 150 155 160
- Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly
 165 170 175
- Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala 180 185 190
- Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu 195 200 205
- Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu 210 225 220
- Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Thr Val Asp Phe Gly Pro 225 230 235 240
- Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro 245 250 255
- His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr 260 265 270
- Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly
 275 280 285
- Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe 290 295 300
- His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly 305 310 315 320
- Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser 325 330 335
- Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile

			340					345					350		
Ser	Lys	Phe 355	Gln	Glu	Val	Pro	Leu 360	Gly	Pro	Leu	Pro	Pro 365	Pro	Ser	Pro
Lys	Met 370	Met	Leu	Gly	Pro	Val 375	Thr	Leu	His	Leu	Val 380	Gly	His	Leu	Leu
Ala 385	Phe	Leu	Asp	Leu	Leu 390	Cys	Pro	Arg	Gly	Pro 395	Ile	His	Ser	Ile	Leu 400
Pro	Met	Thr	Phe	Glu 405	Ala	Val	Lys	Gln	Asp 410	His	Gly	Phe	Met	Leu 415	Tyr
Arg	Thr	Tyr	Met 420	Thr	His	Thr	Ile	Phe 425	Glu	Pro	Thr	Pro	Phe 430	Trp	Val
Pro	Asn	Asn 435	Gly	Val	His	Asp	Arg 440	Ala	Tyr	Val	Met	Val 445	Asp	Gly	Val
Phe	Gln 450	Gly	Val	Val	Glu	Arg 455	Asn	Met	Arg	Asp	Lys 460	Leu	Phe	Leu	Thr
Gly 465	Lys	Leu	Gly	Ser	Lys 470	Leu	Asp	Ile	Leu	Val 475	Glu	Asn	Met	Gly	Arg 480
Leu	Ser	Phe	Gly	Ser 485	Asn	Ser	Ser	Asp	Phe 490	Lys	Gly	Leu	Leu	Lys 495	Pro
Pro	Ile	Leu	Gly 500	Gln	Thr	Ile	Leu	Thr 505	Gln	Trp	Met	Met	Phe 510	Pro	Leu
Lys	Ile	Asp 515	Asn	Leu	Val	Lys	Trp 520	Trp	Phe	Pro	Leu	Gln 525	Leu	Pro	Lys
Trp	Pro 530	Tyr	Pro	Gln	Ala	Pro 535	Ser	Gly	Pro	Thr	Phe 540	Tyr	Ser	Lys	Thr
Phe 545	Pro	Ile	Leu	Gly	Ser 550	Val	Gly	Asp	Thr	Phe 555	Leu	Tyr	Leu	Pro	Gly 560
Trp	Thr	Lys	Gly	Gln 565	Val	Trp	Ile	Asn	Gly 570	Phe	Asn	Leu	Gly	Arg 575	Tyr
Trp	Thr	Lys	Gln 580	Gly	Pro	Gln	Gln	Thr 585	Leu	Tyr	Val	Pro	Arg 590	Phe	Leu
Leu	Phe	Pro 595	Arg	Gly	Ala	Leu	Asn 600	Lys	Ile	Thr	Leu	Leu 605	Glu	Leu	Glu
Asp	Val 610	Pro	Leu	Gln	Pro	Gln 615	Val	Gln	Phe	Leu	Asp 620	Lys	Pro	Ile	Leu

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala 625 630 635 640	
Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His 645 650	
<210> 178 <211> 24 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 178 tggctactcc aagaccctgg catg	24
<210> 179 <211> 24 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 179 tggacaaatc cccttgctca gccc	24
<210> 180 <211> 50 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 180 gggcttcacc gaagcagtgg acctttattt tgaccacctg atgtccaggg	50
<210> 181 <211> 22 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 181	22

```
<210> 182
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 182
                                                                   24
tggcacccag aatggtgttg gctc
<210> 183
<211> 50
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 183
                                                                   50
cgagatgtca tcagcaagtt ccaggaagtt cctttgggac ctttacctcc
<210> 184
<211> 1947
<212> DNA
<213> Homo sapiens
<400> 184
qctttqaaca cqtctqcaaq cccaaaqttq aqcatctqat tggttatgag gtatttgagt 60
qcacccacaa tatqqcttac atqttqaaaa aqcttctcat cagttacata tccattattt 120
gtgtttatgg ctttatctgc ctctacactc tcttctggtt attcaggata cctttgaagg 180
aatattettt egaaaaagte agagaagaga geagttttag tgacatteea gatgteaaaa 240
acgattttgc gttccttctt cacatggtag accagtatga ccagctatat tccaagcgtt 300
ttqqtqtqtt cttqtcaqaa qttaqtqaaa ataaacttag ggaaattagt ttgaaccatg 360
aqtqqacatt tqaaaaactc aqqcaqcaca tttcacqcaa cgcccaggac aagcaggagt 420
tgcatctgtt catgctgtcg ggggtgcccg atgctgtctt tgacctcaca gacctggatg 480
tgctaaagct tgaactaatt ccagaagcta aaattcctgc taagatttct caaatgacta 540
acctccaaqa qctccacctc tgccactgcc ctgcaaaagt tgaacagact gcttttagct 600
ttcttcgcga tcacttgaga tgccttcacg tgaagttcac tgatgtggct gaaattcctg 660
cctgggtgta tttgctcaaa aaccttcgag agttgtactt aataggcaat ttgaactctg 720
aaaacaataa gatgatagga cttgaatctc tccgagagtt gcggcacctt aagattctcc 780
acqtqaaqaq caatttqacc aaaqttccct ccaacattac agatgtggct ccacatctta 840
caaagttagt cattcataat gacggcacta aactcttggt actgaacagc cttaagaaaa 900
tgatgaatgt cgctgagctg gaactccaga actgtgagct agagagaatc ccacatgcta 960
ttttcagcct ctctaattta caggaactgg atttaaagtc caataacatt cgcacaattg 1020
aggaaatcat cagtttccag catttaaaac gactgacttg tttaaaatta tggcataaca 1080
aaattgttac tattcctccc tctattaccc atgtcaaaaa cttggagtca ctttatttct 1140
ctaacaacaa gctcgaatcc ttaccagtgg cagtatttag tttacagaaa ctcagatgct 1200
tagatgtgag ctacaacaac atttcaatga ttccaataga aataggattg cttcagaacc 1260
tgcagcattt gcatatcact gggaacaaag tggacattct gccaaaacaa ttgtttaaat 1320
```

```
gcataaagtt gaggactttg aatctgggac agaactgcat cacctcactc ccagagaaag 1380
ttggtcagct ctcccagctc actcagctgg agctgaaggg gaactgcttg gaccgcctgc 1440
cageceaget gggceagtgt eggatgetea agaaaagegg gettgttgtg gaagateaee 1500
tttttgatac cctgccactc gaagtcaaag aggcattgaa tcaagacata aatattccct 1560
ttgcaaatgg gatttaaact aagataatat atgcacagtg atgtgcagga acaacttcct 1620
agattgcaag tgctcacgta caagttatta caagataatg cattttagga gtagatacat 1680
cttttaaaat aaaacagaga ggatgcatag aaggctgata gaagacataa ctgaatgttc 1740
aatgtttgta gggttttaag tcattcattt ccaaatcatt tttttttttc ttttggggaa 1800
agggaaggaa aaattataat cactaatctt ggttcttttt aaattgtttg taacttggat 1860
qctqccqcta ctqaatqttt acaaattqct tqcctqctaa aqtaaatqat taaattqaca 1920
ttttcttact aaaaaaaaa aaaaaaa
<210> 185
<211> 501
<212> PRT
<213> Homo sapiens
<400> 185
Met Ala Tyr Met Leu Lys Lys Leu Leu Ile Ser Tyr Ile Ser Ile Ile
Cys Val Tyr Gly Phe Ile Cys Leu Tyr Thr Leu Phe Trp Leu Phe Arg
                                 25
Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu Glu Ser Ser
Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Leu Leu His
                        . 55
Met Val Asp Gln Tyr Asp Gln Leu Tyr Ser Lys Arg Phe Gly Val Phe
 65
                     70
                                         75
Leu Ser Glu Val Ser Glu Asn Lys Leu Arg Glu Ile Ser Leu Asn His
Glu Trp Thr Phe Glu Lys Leu Arg Gln His Ile Ser Arg Asn Ala Gln
                                105
Asp Lys Gln Glu Leu His Leu Phe Met Leu Ser Gly Val Pro Asp Ala
        115
                            120
                                                125
Val Phe Asp Leu Thr Asp Leu Asp Val Leu Lys Leu Glu Leu Ile Pro
                        135
Glu Ala Lys Ile Pro Ala Lys Ile Ser Gln Met Thr Asn Leu Gln Glu
145
                    150
                                        155
                                                             160
Leu His Leu Cys His Cys Pro Ala Lys Val Glu Gln Thr Ala Phe Ser
                165
                                    170
Phe Leu Arg Asp His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val
```

185

- Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu 195 200 205
- Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu 210 215 220
- Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser 225 230 235 240
- Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu 245 250 255
- Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn 260 265 270
- Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys 275 280 285
- Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln 290 295 300
- Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile 305 310 315 320
- Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn 325 330 335
- Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu 340 345 350
- Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val
- Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile 370 375 380
- Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu 385 390 395 400
- His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys 405 410 415
- Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser 420 425 430
- Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu
 435 440 445
- Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg 450 455 460
- Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

465	470	475	480
Leu Pro Leu Glu Val 485	Lys Glu Ala Le	eu Asn Gln Asp Ile As 490	sn Ile Pro 495
Phe Ala Asn Gly Ile 500			
<210> 186 <211> 21 <212> DNA <213> Artificial Sec	quence		
<220> <223> Description of oligonucleotic		equence: Synthetic	
<400> 186 cctccctcta ttacccat	gt c		21
<210> 187 <211> 24 <212> DNA <213> Artificial Sec	quence		
<220> <223> Description of oligonucleotic		equence: Synthetic	
<400> 187 gaccaacttt ctctgggag	gt gagg		24
<210> 188 <211> 47 <212> DNA <213> Artificial Sec	quence		
<220> <223> Description of oligonucleotic		equence: Synthetic	
<400> 188 gtcactttat ttctctaac	ca acaagctcga a	atccttacca gtggcag	47
<210> 189 <211> 2917 <212> DNA <213> Homo sapiens			
actttttta tttctttt	tt tccatctctg	gcatttecat tecttttea ggccagettg ggatectag etgtgtttgg ggtttette	g ccgccctggg 120

```
acattggcat tgcttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgctt 240
gcacttatct gcctaggtac atcgaagtct tttgacctcc atacagtgat tatgcctgtc 300
atcgctggtg gtatcctggc ggccttgctc ctgctgatag ttgtcgtgct ctgtctttac 360
ttcaaaatac acaacgcgct aaaagctgca aaggaacctg aagctgtggc tgtaaaaaat 420
cacaacccag acaaggtgtg gtgggccaag aacagccagg ccaaaaccat tgccacggag 480
tettgteetg ceetgeagtg etgtgaagga tatagaatgt gtgceagttt tgatteeetg 540
ccaccttqct qttqcqacat aaatqagggc ctctgagtta ggaaaggctc ccttctcaaa 600
gcagagccct gaagacttca atgatgtcaa tgaggccacc tgtttgtgat gtgcaggcac 660
agaagaaagg cacagctccc catcagtttc atggaaaata actcagtgcc tgctgggaac 720
cagctgctgg agatccctac agagagcttc cactgggggc aacccttcca ggaaggagtt 780
qqqqaqaqaq aaccctcact gtggggaatg ctgataaacc agtcacacag ctgctctatt 840
ctcacacaaa tctacccctt gcgtggctgg aactgacgtt tccctggagg tgtccagaaa 900
getgatgtaa cacagageet ataaaagetg teggteetta aggetgeeca gegeettgee 960
aaaatggagc ttgtaagaag gctcatgcca ttgaccctct taattctctc ctgtttggcg 1020
gagctgacaa tggcggaggc tgaaggcaat gcaagctgca cagtcagtct agggggtgcc 1080
aatatggcag agacccacaa agccatgatc ctgcaactca atcccagtga gaactgcacc 1140
tggacaatag aaagaccaga aaacaaaagc atcagaatta tetttteeta tgtecagett 1200
gatccagatg gaagctgtga aagtgaaaac attaaagtct ttgacggaac ctccagcaat 1260
gggcctctgc tagggcaagt ctgcagtaaa aacgactatg ttcctgtatt tgaatcatca 1320
tccagtacat tgacgtttca aatagttact gactcagcaa gaattcaaag aactgtcttt 1380
gtettetaet aettettete teetaacate tetatteeaa aetgtggegg ttaeetggat 1440
accttggaag gatccttcac cagccccaat tacccaaagc cgcatcctga gctggcttat 1500
tgtgtgtggc acatacaagt ggagaaagat tacaagataa aactaaactt caaagagatt 1560
ttcctagaaa tagacaaaca gtgcaaattt gattttcttg ccatctatga tggcccctcc 1620
accaactetg geetgattgg acaagtetgt ggeegtgtga etcecacett egaategtea 1680
tcaaactctc tqactgtcgt gttgtctaca gattatgcca attcttaccg gggattttct 1740
qcttcctaca cctcaattta tgcagaaaac atcaacacta catctttaac ttgctcttct 1800
gacaggatga gagttattat aagcaaatcc tacctagagg cttttaactc taatgggaat 1860
aacttgcaac taaaagaccc aacttgcaga ccaaaattat caaatgttgt ggaattttct 1920
gtccctctta atggatgtgg tacaatcaga aaggtagaag atcagtcaat tacttacacc 1980
aatataatca cettttetqe ateeteaact tetgaagtga teaccegtea gaaacaacte 2040
cagattattg tgaagtgtga aatgggacat aattctacag tggagataat atacataaca 2100
gaagatgatg taatacaaag tcaaaatgca ctgggcaaat ataacaccag catggctctt 2160
tttgaatcca attcatttga aaagactata cttgaatcac catattatgt ggatttgaac 2220
caaactettt ttqttcaaqt tagtetgeac aceteagate caaatttggt ggtgtttett 2280
gatacctgta gagcctctcc cacctctgac tttgcatctc caacctacga cctaatcaag 2340
agtggatgta gtcgagatga aacttgtaag gtgtatccct tatttggaca ctatgggaga 2400
ttccagttta atgcctttaa attcttgaga agtatgagct ctgtgtatct gcagtgtaaa 2460
gttttgatat gtgatagcag tgaccaccag tctcgctgca atcaaggttg tgtctccaga 2520
agcaaacqaq acatttcttc atataaatgg aaaacagatt ccatcatagg acccattcgt 2580
ctgaaaaggg atcgaagtgc aagtggcaat tcaggatttc agcatgaaac acatgcggaa 2640
gaaactecaa accageettt caacagtgtg catetgtttt eetteatggt tetagetetg 2700
aatgtggtga ctgtagcgac aatcacagtg aggcattttg taaatcaacg ggcagactac 2760
aaataccaga agctgcagaa ctattaacta acaggtccaa ccctaagtga gacatgtttc 2820
tccaggatgc caaaggaaat gctacctcgt ggctacacat attatgaata aatgaggaag 2880
ggcctgaaag tgacacacag gcctgcatgt aaaaaaa
```

<210> 190

<211> 607

<212> PRT

<213> Homo sapiens

- Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser 1 5 10 15
- Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys 20 25 30
- Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met 35 40 45
- Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg
- Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp 65 70 75 80
- Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr 85 90 95
- Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr
 100 105 110
- Val Pro Val Phe Glu Ser Ser Ser Ser Thr Leu Thr Phe Gln Ile Val 115 120 125
- Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe 130 135 140
- Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr 145 150 155 160
- Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu 165 170 175
- Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile 180 185 190
- Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys 195 200 205
- Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu 210 215 220
- Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser 225 230 235 240
- Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg 245 250 255
- Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr 260 265 270
- Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys 275 280 285

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys 290 295 300

Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val 305 310 315 320

Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile 325 330 335

Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val 340 345 350

Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly 355 360 365

His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile 370 375 380

Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe 385 390 395 400

Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val 405 410 415

Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp 420 425 430

Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser 435 440 445

Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg 450 455 460

Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe 465 470 475 480

Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu 485 490 495

Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys 500 505 510

Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys 515 520 525

Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg 530 535 540

Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu 545 550 555 560

Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

					565					570					575		
	Leu	Ala	Leu	Asn 580	Val	Val	Thr	Val	Ala 585	Thr	Ile	Thr	Val	Arg 590	His	Phe	
	Val	Asn	Gln 595	Arg	Ala	Asp	Tyr	Lys 600	Tyr	Gln	Lys	Leu	Gln 605	Asn	Tyr		
•	<212	.> 21 !> Di	l NA	icial	l Sec	quenc	ce										
	<220 <223	3 > De			on of eotid			cial	Seq	ience	e: Sy	ynthe	etic				
)> 19															0.1
	tctc	tati	ccc a	aaact	tgtgg	gc g											21
)> 19															
		l> 22 2> Di															
				icial	l Sec	queno	ce										
	<220 <223	3 > De		_	on of			cial	Seq	uence	e: Sy	ynth:	etic				
	<400)> 19	92														
	tttg	gatga	acg a	attc	gaagg	gt gg	3										22
	<210)> 19	93														
		L> 4'															
		2 > D1 3 > A1		icial	l Sec	nueno	ce										
	~2.2.	, , , , , ,			- 500	140											
	<220		ogar:	inti	on of	= 7\ ~ +	-ifi/	ai al	Sec	ience	a . G	ent he	etic				
	<423				eotic			JIAI	seqi	dence	z. Dj	YIICII	SCIC				
)> 19															
	ggaa	iggat	taa t	ttcad	ccago	c c	caati	tacco	c aa	agcc	gcat	cct	gagc				47
)> 19													•		
		l> 2: 2> Di															
				sapie	ens												
	-40r)> 19	94														
				cage	gctco	c ga	aggc	cgcgg	g ga	gcct	gcag	agag	ggaca	agc	cggc	ctgcgc	60
	cggg	gacat	tgc 9	ggcc	ccago	ga go	ctcc	ccag	g ct	cgcgt	ttcc	cgti	tgct	gct ·	gttg	tgttg	120
	ctgo	etgei	tgc (cgcc	gccgc	c gt	tgcc	ctgc	ca	cage	gcca	cgc	gctt	cga	cccc	acctgg	180

```
gagtccctgg acgcccgcca gctgcccgcg tggtttgacc aggccaagtt cggcatcttc 240
atccactggg gagtgttttc cgtgcccagc ttcggtagcg agtggttctg gtggtattgg 300
caaaaggaaa agataccgaa gtatgtggaa tttatgaaag ataattaccc tcctagtttc 360
aaatatgaag attttggacc actatttaca gcaaaatttt ttaatgccaa ccagtgggca 420
qatatttttc aqqcctctqq tqccaaatac attqtcttaa cttccaaaca tcatqaaqqc 480
tttaccttgt gggggtcaga atattcgtgg aactggaatg ccatagatga ggggcccaag 540
agggacattg tcaaggaact tgaggtagcc attaggaaca gaactgacct gcgttttgga 600
ctgtactatt ccctttttga atggtttcat ccgctcttcc ttgaggatga atccagttca 660
ttccataaqc qqcaatttcc agtttctaag acattgccag agctctatga gttagtgaac 720
aactatcagc ctgaggttct gtggtcggat ggtgacggag gagcaccgga tcaatactgg 780
aacagcacag gcttcttggc ctggttatat aatgaaagcc cagttcgggg cacagtagtc 840
accaatqate qttqqqqaqe tqqtaqcate tqtaagcatg gtggetteta tacctgcagt 900
gatcgttata acccaggaca tcttttgcca cataaatggg aaaactgcat gacaatagac 960
aaactgtcct ggggctatag gagggaagct ggaatctctg actatcttac aattgaagaa 1020
ttqqtqaaqc aacttqtaqa qacaqtttca tgtggaggaa atcttttgat gaatattggg 1080
cccacactag atggcaccat ttctgtagtt tttgaggagc gactgaggca agtggggtcc 1140
tggctaaaag tcaatggaga agctatttat gaaacctata cctggcgatc ccagaatgac 1200
actgtcaccc cagatgtgtg gtacacatcc aagcctaaag aaaaattagt ctatgccatt 1260
tttcttaaat qqcccacatc aqqacaqctq ttccttgqcc atcccaaagc tattctgggg 1320
gcaacagagg tgaaactact gggccatgga cagccactta actggatttc tttggagcaa 1380
aatggcatta tggtagaact gccacagcta accattcatc agatgccgtg taaatggggc 1440
tgggctctag ccctaactaa tgtgatctaa agtgcagcag agtggctgat gctgcaagtt 1500
atgtctaagg ctaggaacta tcaggtgtct ataattgtag cacatggaga aagcaatgta 1560
aactggataa gaaaattatt tggcagttca gccctttccc tttttcccac taaatttttc 1620
ttaaattacc catgtaacca ttttaactct ccagtgcact ttgccattaa agtctcttca 1680
cattgatttg tttccatgtg tgactcagag gtgagaattt tttcacatta tagtagcaag 1740
gaattggtgg tattatggac cgaactgaaa attttatgtt gaagccatat cccccatgat 1800
tatataqtta tqcatcactt aatatqqqqa tattttctqq qaaatqcatt qctaqtcaat 1860
tttttttttttqt qccaacatca taqaqtqtat ttacaaaatc ctaqatqqca taqcctacta 1920
cacacctaat qtqtatqqta taqactqttq ctcctaqqct acagacatat acagcatgtt 1980
actgaatact qtaqqcaata qtaacaqtgq tatttgtata tcgaaacata tggaaacata 2040
qaqaaqqtac aqtaaaaata ctqtaaaaata aatgqtgcac ctgtataggg cacttaccac 2100
gaatggaget tacaggactg gaagttgete tgggtgagte agtgagtgaa tgtgaaggee 2160
taggacatta ttgaacactg ccagacgtta taaatactgt atgcttaggc tacactacat 2220
ttataaaaaa aagtttttct ttcttcaatt ataaattaac ataagtgtac tgtaacttta 2280
caaacgtttt aatttttaaa acctttttgg ctcttttgta ataacactta gcttaaaaca 2340
taaactcatt gtgcaaatgt aa
                                                                  2362
<210> 195
<211> 467
<212> PRT
<213> Homo sapiens
```

```
<400> 195
```

```
Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu
```

Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr 25

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala 40 35

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe 50 55 60

Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys
65 70 75 80

Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro 85 90 95

Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe 100 105 110

Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr 115 120 125

Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser 130 135 140

Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp 145 150 155 160

Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg 165 170 175

Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu 180 185 190

Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys 195 200 205

Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val 210 215 220

Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser 225 230 235 240

Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr
245 250 255

Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly 260 265 270

Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro 275 280 285

His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr 290 295 300

Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val 305 310 315 320

Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn 325 330 335

<210> 198

Ile Gly	/ Pro	Thr 340	Leu	Asp	Gly	Thr	Ile 345	Ser	Val	Val	Phe	Glu 350	Glu	Arg	
Leu Arg	g Gln 355		Gly	Ser	Trp	Leu 360	Lys	Val	Asn	Gly	Glu 365	Ala	Ile	Tyr	
Glu Thi		Thr	Trp	Arg	Ser 375	Gln	Asn	Asp	Thr	Val 380	Thr	Pro	Asp	Val	
Trp Ty1	Thr	Ser	Lys	Pro 390	Lys	Glu	Lys	Leu	Val 395	Tyr	Ala	Ile	Phe	Leu 400	
Lys Tr) Pro	Thr	Ser 405	Gly	Gln	Leu	Phe	Leu 410	Gly	His	Pro	Lys	Ala 415	Ile	
Leu Gly	/ Ala	Thr 420	Glu	Val	Lys	Leu	Leu 425	Gly	His	Gly	Gln	Pro 430	Leu	Asn	
Trp Ile	e Ser 435		Glu	Gln	Asn	Gly 440	Ile	Met	Val	Glu	Leu 445	Pro	Gln	Leu	
Thr Ile		Gln	Met	Pro	Cys 455	Lys	Trp	Gly	Trp	Ala 460	Leu	Ala	Leu	Thr	
Asn Val	l Ile													-	
<210 > 3 <211 > 3 <212 > 1 <213 > 3	23 ONA	icia	l Se	quen	ce										
<220> <223> I	Descr oligo	_				cial	Seq	uence	e: S	ynth	etic				
<400> i		aggc	caag	tt c	3 9										23
<210 > 3 <211 > 3 <212 > 1 <213 > 3	24 ONA	icia	l Se	quen	ce										
<220> <223> I	Descr oligo	_				cial	Seq	uenc	e: S	ynth	etic				
<400> 3		tcaa	ggaa	ga g	egg										24

```
<211> 24
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Synthetic
     oligonucleotide probe
<400> 198
                                                                  24
aacttgcagc atcagccact ctgc
<210> 199
<211> 45
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 199
ttccgtgccc agcttcggta gcgagtggtt ctggtggtat tggca
                                                                  45
<210> 200
<211> 2372
<212> DNA
<213> Homo sapiens
<400> 200
agcagggaaa tccggatgtc tcggttatga agtggagcag tgagtgtgag cctcaacata 60
qttccaqaac tctccatccg gactagttat tgagcatctg cctctcatat caccagtggc 120
catctgaggt gtttccctgg ctctgaaggg gtaggcacga tggccaggtg cttcagcctg 180
gtgttgcttc tcacttccat ctggaccacg aggctcctgg tccaaggctc tttgcgtgca 240
gaagagettt ccatccaggt gtcatgcaga attatgggga tcaccettgt gagcaaaaag 300
qcqaaccaqc aqctqaattt cacaqaagct aaggaggcct gtaggctgct gggactaagt 360
ttggccggca aggaccaagt tgaaacagcc ttgaaagcta gctttgaaac ttgcagctat 420
ggctgggttg gagatggatt cgtggtcatc tctaggatta gcccaaaccc caagtgtggg 480
aaaaatgggg tgggtgtcct gatttggaag gttccagtga gccgacagtt tgcagcctat 540
tgttacaact catctgatac ttggactaac tcgtgcattc cagaaattat caccaccaaa 600
gatcccatat tcaacactca aactgcaaca caaacaacag aatttattgt cagtgacagt 660
acctactcgg tggcatcccc ttactctaca atacctgccc ctactactac tcctcctgct 720
ccagcttcca cttctattcc acggagaaaa aaattgattt gtgtcacaga agtttttatg 780
gaaactagca ccatgtctac agaaactgaa ccatttgttg aaaataaagc agcattcaag 840
aatgaagetg etgggtttgg aggtgteece aeggetetge tagtgettge teteetette 900
tttggtgctg cagctggtct tggattttgc tatgtcaaaa ggtatgtgaa ggccttccct 960
tttacaaaca agaatcagca gaaggaaatg atcgaaacca aagtagtaaa ggaggagaag 1020
gccaatgata gcaaccctaa tgaggaatca aagaaaactg ataaaaaccc agaagagtcc 1080
aagagtccaa gcaaaactac cgtgcgatgc ctggaagctg aagtttagat gagacagaaa 1140
tgaggagaca cacctgaggc tggtttcttt catgctcctt accctgcccc agctggggaa 1200
atcaaaaqqq ccaaagaacc aaagaagaaa gtccaccctt ggttcctaac tggaatcagc 1260
traggarter cattegarta tegagtera caaagagaat greetteter ttattetaar 1320
cctgtctgga tcctatcctc ctacctccaa agcttcccac ggcctttcta gcctggctat 1380
gtcctaataa tatcccactg ggagaaagga gttttgcaaa gtgcaaggac ctaaaacatc 1440
```

130

```
tcatcagtat ccagtggtaa aaaggcctcc tggctgtctg aggctaggtg ggttgaaagc 1500
caaqqaqtca ctgagaccaa ggctttctct actgattccg cagctcagac cctttcttca 1560
qctctqaaaq aqaaacacgt atcccacctg acatgtcctt ctgagcccgg taagagcaaa 1620
agaatggcag aaaagtttag cccctgaaag ccatggagat tctcataact tgagacctaa 1680
tctctgtaaa gctaaaataa agaaatagaa caaggctgag gatacgacag tacactgtca 1740
gcagggactg taaacacaga cagggtcaaa gtgttttctc tgaacacatt gagttggaat 1800
cactgtttag aacacacac cttacttttt ctggtctcta ccactgctga tattttctct 1860
aggaaatata cttttacaag taacaaaaat aaaaactctt ataaatttct atttttatct 1920
gagttacaga aatgattact aaggaagatt actcagtaat ttgtttaaaa agtaataaaa 1980
ttcaacaaac atttgctgaa tagctactat atgtcaagtg ctgtgcaagg tattacactc 2040
tqtaattqaa tattattcct caaaaaattg cacatagtag aacgctatct gggaagctat 2100
ttttttcagt tttgatattt ctagcttatc tacttccaaa ctaattttta tttttgctga 2160
qactaatctt attcattttc tctaatatgg caaccattat aaccttaatt tattattaac 2220
atacctaaqa aqtacattqt tacctctata taccaaagca cattttaaaa gtgccattaa 2280
caaatgtatc actagccctc ctttttccaa caagaaggga ctgagagatg cagaaatatt 2340
tgtgacaaaa aattaaagca tttagaaaac tt
<210> 201
<211> 322
<212> PRT
<213> Artificial sequence
<220>
<223> Synthetic protein
<400> 201
Met Ala Arg Cys Phe Ser Leu Val Leu Leu Thr Ser Ile Trp Thr
  1
Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
                                 25
Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
                     70
Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
                 85
Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
                            120
Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile
```

<211> 22 <212> DNA

<213> Artificial Sequence

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr 145 150 155 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser 165 170 Thr Ile Pro Ala Pro Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser 185 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu 195 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala 215 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu 235 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Gly Leu Gly Phe 245 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn 265 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala 275 280 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala 305 310 315 320 Glu Val <210> 202 <211> 24 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe <400> 202 gagettteca tecaggtgte atge <210> 203

```
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 203
                                                                    22
gtcagtgaca gtacctactc gg
<210> 204
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 204
                                                                    24
tggagcagga ggagtagtag tagg
<210> 205
<211> 50
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt
                                                                    50
<210> 206
<211> 1620
<212> DNA
<213> Homo sapiens
<220>
<221> modified base
<222> (973)
<223> a, t, c or g
<220>
<221> modified_base
<222> (977)
<223> a, t, c or g
<220>
<221> modified base
<222> (996)
<223> a, t, c or g
<220>
<221> modified base
```

```
<222> (1003)
<223> a, t, c or g
<400> 206
agatggcggt cttggcacct ctaattgctc tcgtgtattc ggtgccgcga ctttcacgat 60
ggctcgccca accttactac cttctgtcgg ccctgctctc tgctgccttc ctactcgtga 120
ggaaactgcc gccgctctgc cacggtctgc ccacccaacg cgaagacggt aacccgtgtg 180
actttqactq qaqaaqaaqtq qaqatcctqa tgtttctcag tgccattgtg atgatgaaga 240
accgcaqatc catcactqtq qaqcaacata taqqcaacat tttcatgttt agtaaagtgg 300
ccaacacaat totttotto cgottggata ttogcatggg cotactttac atcacactot 360
gcatagtgtt cctgatgacg tgcaaacccc ccctatatat gggccctgag tatatcaagt 420
acttcaatqa taaaaccatt gatgaggaac tagaacggga caagagggtc acttggattg 480
tggagttett tgecaattgg tetaatgaet gecaateatt tgeceetate tatgetgaee 540
tctcccttaa atacaactgt acagggctaa attttgggaa ggtggatgtt ggacgctata 600
ctgatgttag tacgcggtac aaagtgagca catcaccct caccaagcaa ctccctaccc 660
tgatcctgtt ccaaggtggc aaggaggcaa tgcggcggcc acagattgac.aagaaaggac 720
gggctgtctc atggaccttc tctgaggaga atgtgatccg agaatttaac ttaaatgagc 780
tataccagcg ggccaagaaa ctatcaaagg ctggagacaa tatccctgag gagcagcctg 840
tggcttcaac ccccaccaca gtgtcagatg gggaaaacaa gaaggataaa taagatcctc 900
actttggcag tgcttcctct cctgtcaatt ccaggctctt tccataacca caagcctgag 960
gctgcagcct ttnattnatg ttttcccttt ggctgngact ggntggggca gcatgcagct 1020
tctgatttta aagaggcatc tagggaattg tcaggcaccc tacaggaagg cctgccatgc 1080
tgtggccaac tgtttcactg gagcaagaaa gagatctcat aggacggagg gggaaatggt 1140
ttccctccaa gcttgggtca gtgtgttaac tgcttatcag ctattcagac atctccatgg 1200
tttctccatg aaactctgtg gtttcatcat tccttcttag ttgacctgca cagcttggtt 1260
agacctagat ttaaccctaa ggtaagatgc tggggtatag aacgctaaga attttccccc 1320
aaggactett getteettaa geeettetgg ettegtttat ggtetteatt aaaagtataa 1380
gcctaacttt gtcgctagtc ctaaggagaa acctttaacc acaaagtttt tatcattgaa 1440
gacaatattg aacaacccc tattttgtgg ggattgagaa ggggtgaata gaggcttgag 1500
actttccttt gtgtggtagg acttggagga gaaatcccct ggactttcac taaccctctg 1560
acatactccc cacacccagt tgatggcttt ccgtaataaa aagattggga tttccttttg 1620
<210> 207
<211> 296
<212> PRT
<213> Homo sapiens
<400> 207
Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
             20
Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
                                                             80
                                         75
```

Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe
85 90 95

Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met 100 105 110

Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys 115 120 125

Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys 130 135 140

Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val 145 150 155 160

Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile 165 170 175

Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly
180 185 190

Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val 195 200 205

Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln 210 215 220

Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg 225 230 235 240

Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn 245 250 255

Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp 260 265 270

Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser 275 280 285

Asp Gly Glu Asn Lys Lys Asp Lys 290 295

<210> 208

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<400> 208

gcttggatat tcgcatgggc ctac

```
<210> 209
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
     oligonucleotide probe
<400> 209
                                                                   20
tggagacaat atccctgagg
<210> 210
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 210
                                                                   24
aacagttggc cacagcatgg cagg
<210> 211
<211> 50
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 211
ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag
                                                                   50
<210> 212
<211> 1985
<212> DNA
<213> Homo sapiens
<400> 212
ggacageteg eggeeeeega gagetetage egtegaggag etgeetgggg aegtttgeee 60
tggggcccca gcctggcccg ggtcaccctg gcatgaggag atgggcctgt tgctcctggt 120
cccattgctc ctgctgcccg gctcctacgg actgcccttc tacaacggct tctactactc 180
caacagcgcc aacgaccaga acctaggcaa cggtcatggc aaagacctcc ttaatggagt 240
gaagctggtg gtggagacac ccgaggagac cctgttcacc taccaagggg ccagtgtgat 300
cctgccctgc cgctaccgct acgagccggc cctggtctcc ccgcggcgtg tgcgtgtcaa 360
atggtggaag ctgtcggaga acggggcccc agagaaggac gtgctggtgg ccatcgggct 420
gaggcaccgc tcctttgggg actaccaagg ccgcgtgcac ctgcggcagg acaaagagca 480
tgacgteteg etggagatee aggatetgeg getggaggae tatgggegtt accgetgtga 540
ggtcattgac gggctggagg atgaaagcgg tctggtggag ctggagctgc ggggtgtggt 600
```

```
ctttccttac cagtccccca acgggcgcta ccagttcaac ttccacgagg gccagcaggt 660
ctgtgcagag caggctgcgg tggtggcctc ctttgagcag ctcttccggg cctgggagga 720
gggcctggac tggtgcaacg cgggctggct gcaggatgct acggtgcagt accccatcat 780
gttgccccgg cagccctgcg gtggcccagg cctggcacct ggcgtgcgaa gctacggccc 840
ecgecacege egectgeace getatgatgt attetgette getactgeee teaaggggeg 900
ggtgtactac ctggagcacc ctgagaagct gacgctgaca gaggcaaggg aggcctgcca 960
ggaagatgat gccacgatcg ccaaggtggg acagctcttt gccgcctgga agttccatgg 1020
cctggaccgc tgcgacgctg gctggctggc agatggcagc gtccgctacc ctgtggttca 1080
cccgcatcct aactgtgggc ccccagagcc tggggtccga agctttggct tccccgaccc 1140
quadaqueqe ttqtacqqtq tttactqcta ccqccagcac taggacctgg ggccctcccc 1200
tgccgcattc cctcactggc tgtgtattta ttgagtggtt cgttttccct tgtgggttgg 1260
agccatttta actgttttta tacttctcaa tttaaatttt ctttaaacat tttttacta 1320
ttttttgtaa agcaaacaga acccaatgcc tccctttgct cctggatgcc ccactccagg 1380
aatcatqctt qctcccctqq qccatttqcq qttttqtqqq cttctggagg gttccccgcc 1440
atccapqctq gtctccctcc cttaaggagg ttggtgccca gagtgggcgg tggcctgtct 1500
agaatgeege egggagteeg ggcatggtgg gcacagttet ceetgeeect cageetgggg 1560
qaaqaaqaqq qcctcggggg cctccggagc tgggctttgg gcctctcctg cccacctcta 1620
cttctctqtq aagccgctga ccccagtctg cccactgagg ggctagggct ggaagccagt 1680
tctaggcttc caggcgaaat ctgagggaag gaagaaactc ccctccccgt tccccttccc 1740
ctctcggttc caaagaatct gttttgttgt catttgtttc tcctgtttcc ctgtgtgggg 1800
aggggccctc aggtgtgtgt actttggaca ataaatggtg ctatgactgc cttccgccaa 1860
1985
aaaaa
<210> 213
<211> 360
<212> PRT
<213> Homo sapiens
<400> 213
Met Gly Leu Leu Leu Val Pro Leu Leu Leu Pro Gly Ser Tyr
                                   10
Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp
                               25
Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys
        35
Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala
                       55
Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser
 65
                   70
                                      75
Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala
```

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe

105

		115					120					125			
Val	Ser 130	Leu	Glu	Ile	Gln	Asp 135	Leu	Arg	Leu	Glu	Asp 140	Tyr	Gly	Arg	Tyr
Arg 145	Cys	Glu	Val	Ile	Asp 150	Gly	Leu	Glu	Asp	Glu 155	Ser	Gly	Leu	Val	Glu 160
Leu	Glu	Leu	Arg	Gly 165	Val	Val	Phe	Pro	Tyr 170	Gln	Ser	Pro	Asn	Gly 175	Arg
Tyr	Gln	Phe	Asn 180	Phe	His	Glu	Gly	Gln 185	Gln	Val	Cys	Ala	Glu 190	Gln	Ala
Ala	Val	Val 195	Ala	Ser	Phe	Glu	Gln 200	Leu	Phe	Arg	Ala	Trp 205	Glu	Glu	Gly
Leu	Asp 210	Trp	Cys	Asn	Ala	Gly 215	Trp	Leu	Gln	Asp	Ala 220	Thr	Val	Gln	Tyr
Pro 225	Ile	Met	Leu	Pro	Arg 230	Gln	Pro	Cys	Gly	Gly 235	Pro	Gly	Leu	Ala	Pro 240
Gly	Val	Arg	Ser	Tyr 245	Gly	Pro	Arg	His	Arg 250	Arg	Leu	His	Arg	Tyr 255	Asp
Val	Phe	Cys	Phe 260	Ala	Thr	Ala	Leu	Lys 265	Gly	Arg	Val	Tyr	Tyr 270	Leu	Glu
His	Pro	Glu 275	Lys	Leu	Thr	Leu	Thr 280	Glu	Ala	Arg	Glu	Ala 285	Cys	Gln	Glu
Asp	Asp 290	Ala	Thr	Ile	Ala	Lys 295	Val	Gly	Gln	Leu	Phe 300	Ala	Ala	Trp	Lys
Phe 305	His	Gly	Leu	Asp	Arg 310	Cys	Asp	Ala	Gly	Trp 315	Leu	Ala	Asp	Gly	Ser 320
Val	Arg	Tyr	Pro	Val 325	Val	His	Pro	His	Pro 330	Asn	Cys	Gly	Pro	Pro 335	Glu
Pro	Gly	Val	Arg 340	Ser	Phe	Gly	Phe	Pro 345	Asp	Pro	Gln	Ser	Arg 350	Leu	Tyr
Gly	Val	Tyr 355	Cys	Tyr	Arg	Gln	His 360								
<211 <212	0> 23 L> 18 2> Di 3> Ai	S NA	icial	l Sed	quenc	ce									
<220)>														

<223>	Description of Artificial oligonucleotide probe	Sequence:	Synthetic	
<400> tgctto	214 egeta etgeeete			. 18
<210><211><212><213>	18		·	
<220> <223>	Description of Artificial oligonucleotide probe	Sequence:	Synthetic	
<400> ttccct	215 tgtg ggttggag			18
<210><211><212><212><213>	18			
<220> <223>	Description of Artificial oligonucleotide probe	Sequence:	Synthetic	
<400> agggct	216 Eggaa gccagttc			18
<210><211><211><212><213>	18			
<220> <223>	Description of Artificial oligonucleotide probe	Sequence:	Synthetic	
<400> agccag	217 gtgag gaaatgcg			18
<210><211><212><212><213>	24			
<220> <223>	Description of Artificial oligonucleotide probe	Sequence:	Synthetic	
<400>	218 aaagt acacacacct gagg			24

```
<210> 219
<211> 45
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
     oligonucleotide probe
<400> 219
                                                                45
gatgccacga tcgccaaggt gggacagctc tttgccgcct ggaag
<210> 220
<211> 1503
<212> DNA
<213> Homo sapiens
<400> 220
ggagagcgga gcgaagctgg ataacagggg accgatgatg tggcgaccat cagttctgct 60
gettetgttg etactgagge aeggggecca ggggaageca teeccagaeg eaggeeetca 120
tggccagggg agggtgcacc agggggcccc cctgagcgac gctccccatg atgacgccca 180
cgggaacttc cagtacgacc atgaggcttt cctgggacgg gaagtggcca aggaattcga 240
ccaactcacc ccagaggaaa gccaggcccg tctggggcgg atcgtggacc gcatggaccg 300
cgcgggggac ggcgacggct gggtgtcgct ggccgagctt cgcgcgtgga tcgcgcacac 360
qcaqcaqcqq cacatacgqq actcggtgag cgcggcctgg gacacgtacg acacggaccg 420
cgacgggcgt gtgggttggg aggagctgcg caacgccacc tatggccact acgcgcccgg 480
tgaagaattt catgacgtgg aggatgcaga gacctacaaa aagatgctgg ctcgggacga 540
geggegttte egggtggeeg accaggatgg ggaetegatg gecaetegag aggagetgae 600
agecttectg cacceegagg agttecetea catgegggae ategtgattg etgaaaceet 660
ggaggacctg gacagaaaca aagatggcta tgtccaggtg gaggagtaca tcgcggatct 720
gtactcagcc gagcctgggg aggaggagcc ggcgtgggtg cagacggaga ggcagcagtt 780
ccgggacttc cgggatctga acaaggatgg gcacctggat gggagtgagg tgggccactg 840
ggtgctgccc cctgcccagg accagcccct ggtggaagcc aaccacctgc tgcacgagag 900
cgacacggac aaggatgggc ggctgagcaa agcggaaatc ctgggtaatt ggaacatgtt 960
tgtgggcagt caggccacca actatggcga ggacctgacc cggcaccacg atgagctgtg 1020
agcaccgcgc acctgccaca gcctcagagg cccgcacaat gaccggagga ggggccgctg 1080
tggtctggcc ccctccctgt ccaggccccg caggaggcag atgcagtccc aggcatcctc 1140
ctgcccctgg gctctcaggg accccctggg tcggcttctg tccctgtcac acccccaacc 1200
ccagggaggg gctgtcatag tcccagagga taagcaatac ctatttctga ctgagtctcc 1260
cageccagae ecagggaece ttggeeceaa geteagetet aagaaeegee ecaaceeete 1320
cagetecaaa tetgageete caccacatag aetgaaaete ceetggeece ageeetetee 1380
tgcctggcct ggcctgggac acctcctctc tgccaggagg caataaaagc cagcgccggg 1440
1503
aaa
<210> 221
<211> 328
<212> PRT
<213> Homo sapiens
<400> 221
```

Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Leu Arg His

1				5					10					15	
Gly	Ala	Gln	Gly 20	Lys	Pro	Ser	Pro	Asp 25	Ala	Gly	Pro	His	Gly 30	Gln	Gly
Arg	Val	His 35	Gln	Ala	Ala	Pro	Leu 40	Ser	Asp	Ala	Pro	His 45	Asp	Asp	Ala
His	Gly 50	Asn	Phe	Gln	Tyr	Asp 55	His	Glu	Ala	Phe	Leu 60	Gly	Arg	Glu	Val
Ala 65	Lys	Glu	Phe	Asp	Gln 70	Leu	Thr	Pro	Glu	Glu 75	Ser	Gln	Ala	Arg	Leu 80
Gly	Arg	Ile	Val	Asp 85	Arg	Met	Asp	Arg	Ala 90	Gly	Asp	Gly	Asp	Gly 95	Trp
Val	Ser	Leu	Ala 100	Glu	Leu	Arg	Ala	Trp 105	Ile	Ala	His	Thr	Gln 110	Gln	Arg
His	Ile	Arg 115	Asp	Ser	Val	Ser	Ala 120	Ala	Trp	Asp	Thr	Туг 125	Asp	Thr	Asp
Arg	Asp 130	Gly	Arg	Val	Gly	Trp 135	Glu	Glu	Leu	Arg	Asn 140	Ala	Thr	Tyr	Gly
His 145	Tyr	Ala	Pro	Gly	Glu 150	Glu	Phe	His	Asp	Val 155	Glu	Asp	Ala	Glu	Thr 160
Tyr	Lys	Lys	Met	Leu 165	Ala	Arg	Asp	Glu	Arg 170	Arg	Phe	Arg	Val	Ala 175	Asp
Gln	Asp	Gly	Asp 180	Ser	Met	Ala	Thr	Arg 185	Glu	Glu	Leu	Thr	Ala 190	Phe	Leu
His	Pro	Glu 195	Glu	Phe	Pro	His	Met 200	Arg	Asp	Ile	Val	Ile 205	Ala	Glu	Thr
Leu	Glu 210	Asp	Leu	Asp	Arg	Asn 215		Asp	Gly	Tyr	Val 220	Gln	Val	Glu	Glu
Tyr 225	Ile	Ala	Asp	Leu	Tyr 230	Ser	Ala	Glu	Pro	Gly 235	Glu	Glu	Glu	Pro	Ala 240
Trp	Val	Gln	Thr	Glu 245	Arg	Gln	Gln	Phe	Arg 250	Asp	Phe	Arg	Asp	Leu 255	Asr
Lys	Asp	Gly	His 260	Leu	Asp	Gly	Ser	Glu 265	Val	Gly	His	Trp	Val 270	Leu	Pro
Pro	Ala	Gln	Asp	Gln	Pro	Leu	Val	Glu	Ala	Asn	His	Leu	Leu	His	Gli

	sp Thr	Asp	Lys	Asp	Gly 295	Arg	Leu	Ser	Lys	Ala 300	Glu	Ile	Leu	Gly	
Asn Tr	cp Asn	Met	Phe	Val 310	Gly	Ser	Gln	Ala	Thr 315	Asn	Tyr	Gly	Glu-	Asp 320	
Leu Th	nr Arg	His	His 325	Asp	Glu	Leu									
<210><211><212><213>	20	icia	l Sed	quen	ce								٠		
<220> <223>	Descr oligo	_				cial	Seq	uence	e: Sy	ynthe	et i c				
<400> cgcag	222 gccct	catg	gcca	3 9								•			20
<210><211><212><212><213>	18	icia	l Se	quen	ce										
<220> <223>	Descr oligo	_				cial	Seq	uence	e: Sy	ynth	etic				
<400> gaaat	223 cctgg	gtaa	ttgg												18
<210><211><212><212><213>	23	icia	l Se	quen	ce										
<220> <223>	Descr oligo						Seq	uence	e: Sy	ynth	etic				
<400> gtgcg	224 eggtg	ctca	cagc	tc a	tc										23
<210><211><212><212><213>	44	icia	l Se	quen	ce										
<220> <223>	Descr oligo						Seq	uenc	e: S	ynth	etic				

```
<400> 225
ccccctgag cgacgetece ccatgatgac gcccacggga actt
                                                                  44
<210> 226
<211> 2403
<212> DNA
<213> Homo sapiens
<400> 226
ggggccttgc cttccgcact cgggcgcagc cgggtggatc tcgagcaggt gcggagcccc 60
gggcggcggg cgcgggtgcg agggatccct gacgcctctg tccctgtttc tttgtcgctc 120
ccagcctgtc tgtcgtcgtt ttggcgcccc cgcctccccg cggtgcgggg ttgcacaccg 180
atcctgggct tcgctcgatt tgccgccgag gcgcctccca gacctagagg ggcgctggcc 240
tggagcagcg ggtcgtctgt gtcctctctc ctctgcgccg cgcccgggga tccgaagggt 300
geggggetet gaggaggtga egeggggge etceegeace etggeettge eegeattete 360
cctctctccc aggtgtgagc agcctatcag tcaccatgtc cgcagcctgg atcccggctc 420
teggeetegg tgtgtgtetg etgetgetge eggggeeege gggeagegag ggageegete 480
ccattgctat cacatgtttt accagaggct tggacatcag gaaagagaaa gcagatgtcc 540
tctgcccagg gggctgccct cttgaggaat tctctgtgta tgggaacata gtatatgctt 600
ctgtatcgag catatgtggg gctgctgtcc acaggggagt aatcagcaac tcagggggac 660
ctgtacgagt ctatagccta cctggtcgag aaaactattc ctcagtagat gccaatggca 720
tccagtctca aatgctttct agatggtctg cttctttcac agtaactaaa ggcaaaagta 780
gtacacagga ggccacagga caagcagtgt ccacagcaca tccaccaaca ggtaaacgac 840
taaagaaaac acccgagaag aaaactggca ataaagattg taaagcagac attgcatttc 900
tgattgatgg aagctttaat attgggcagc gccgatttaa tttacagaag aattttgttg 960
gaaaagtggc tctaatgttg ggaattggaa cagaaggacc acatgtgggc cttgttcaag 1020
ccagtgaaca tcccaaaata gaattttact tgaaaaactt tacatcagcc aaagatgttt 1080
tqtttqccat aaaggaagta ggtttcagag ggggtaattc caatacagga aaagccttga 1140
agcatactgc tcagaaattc ttcacggtag atgctggagt aagaaaaggg atccccaaag 1200
tggtggtggt atttattgat ggttggcctt ctgatgacat cgaggaagca ggcattgtgg 1260
ccagagagtt tggtgtcaat gtatttatag tttctgtggc caagcctatc cctgaagaac 1320
tggggatggt tcaggatgtc acatttgttg acaaggctgt ctgtcggaat aatggcttct 1380
totottacca catgoccaac tggtttggca ccacaaaata cgtaaagcot ctggtacaga 1440
agetgtgeae teatgaacaa atgatgtgea geaagaeetg ttataactea gtgaacattg 1500
cctttctaat tgatggctcc agcagtgttg gagatagcaa tttccgcctc atgcttgaat 1560
ttgtttccaa catagccaag acttttgaaa tctcggacat tggtgccaag atagctgctg 1620
tacagtttac ttatgatcag cgcacggagt tcagtttcac tgactatagc accaaagaga 1680
atgtcctagc tgtcatcaga aacatccgct atatgagtgg tggaacagct actggtgatg 1740
ccatttcctt cactgttaga aatgtgtttg gccctataag ggagagcccc aacaagaact 1800
tectagtaat tgteacagat gggeagteet atgatgatgt ceaaggeeet geagetgetg 1860
cacatgatge aggaatcact atettetetg ttggtgtgge ttgggcacet etggatgace 1920
tgaaagatat ggcttctaaa ccgaaggagt ctcacgcttt cttcacaaga gagttcacag 1980
gattagaacc aattgtttct gatgtcatca gaggcatttg tagagatttc ttagaatccc 2040
agcaataatg gtaacatttt gacaactgaa agaaaaagta caaggggatc cagtgtgtaa 2100
attgtattct cataatactg aaatgcttta gcatactaga atcagataca aaactattaa 2160
gtatgtcaac agccatttag gcaaataagc actcctttaa agccgctgcc ttctggttac 2220
aatttacagt gtactttgtt aaaaacactg ctgaggcttc ataatcatgg ctcttagaaa 2280
ctcaggaaag aggagataat gtggattaaa accttaagag ttctaaccat gcctactaaa 2340
tgtacagata tgcaaattcc atagctcaat aaaagaatct gatacttaga ccaaaaaaaa 2400
                                                                  2403
aaa
```

<211> 550

<212> PRT

<213> Homo sapiens

<400> 227

Met Ser Ala Ala Trp Ile Pro Ala Leu Gly Leu Gly Val Cys Leu Leu 1 5 10 15

Leu Leu Pro Gly Pro Ala Gly Ser Glu Gly Ala Ala Pro Ile Ala Ile 20 25 30

Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val 35 40 45

Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn 50 55 60

Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg 65 70 75 80

Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro 85 90 95

Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln 100 105 110

Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser 115 120 125

Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro 130 135 140

Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys 145 150 155

Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile 165 170 175

Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala 180 185 190

Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln
195 200 205

Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser 210 215 220

Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly 225 230 235 240

Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe 245 250 255

Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val 260 265 270

Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val 275 280 285

Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro 290 295 300

Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys 305 310 315 320

Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp 325 330 335

Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr 340 345 350

His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile 355 360 365

Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg 370 375 380

Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser 385 390 395 400

Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg 405 410 415

Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala
420 425 430

Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp 435 440 445

Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser 450 455 460

Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp 465 470 475 480

Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile
485 490 495

Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met 500 505 510

Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr 515 520 525

Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp 530 535 540

Phe Leu Glu Ser Gln Gln 545 550	
<210> 228 <211> 18 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 228 tggtctcgca caccgatc	18
<210> 229 <211> 18 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 229 ctgctgtcca caggggag	18
<210> 230 <211> 18 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 230 ccttgaagca tactgctc	18
<210> 231 <211> 18 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 231 gagatagcaa tttccgcc	18
<210> 232	

```
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 232
                                                                   18
ttcctcaaga gggcagcc
<210> 233
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 233
                                                                   24
cttggcacca atgtccgaga tttc
<210> 234
<211> 45
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 234
gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg
                                                                   45
<210> 235
<211> 2586
<212> DNA
<213> Homo sapiens
<400> 235
cgccgcgctc ccgcacccgc ggcccgccca ccgcgccgct cccgcatctg cacccgcagc 60
ccggcggcct cccggcggga gcgagcagat ccagtccggc ccgcagcgca actcggtcca 120
gtcggggcgg cggctgcggg cgcagagcgg agatgcagcg gcttggggcc accctgctgt 180
geetgetget ggeggeggeg gteeceaegg eeceeggee egeteegaeg gegaeetegg 240
ctccagtcaa gcccggcccg gctctcagct acccgcagga ggaggccacc ctcaatgaga 300
tgttccgcga ggttgaggaa ctgatggagg acacgcagca caaattgcgc agcgcggtgg 360
aagagatgga ggcagaagaa gctgctgcta aagcatcatc agaagtgaac ctggcaaact 420
tacctcccag ctatcacaat gagaccaaca cagacacgaa ggttggaaat aataccatcc 480
atgtgcaccg agaaattcac aagataacca acaaccagac tggacaaatg gtcttttcag 540
agacaqttat cacatctqtq qqagacqaag aaggcagaaq gagccacgag tgcatcatcg 600
acqaqqactq tqqqcccaqc atgtactgcc agtttgccag cttccagtac acctgccagc 660
catgccgggg ccagaggatg ctctgcaccc gggacagtga gtgctgtgga gaccagctgt 720
```

35

50

```
gtgtctgggg tcactgcacc aaaatggcca ccaggggcag caatgggacc atctgtgaca 780
accagaggga ctgccagccg gggctgtgct gtgccttcca gagaggcctg ctgttccctg 840
tgtgcacacc cctgcccgtg gagggcgagc tttgccatga ccccgccagc cggcttctgg 900
acctcatcac ctgggagcta gagcctgatg gagccttgga ccgatgccct tgtgccagtg 960
gcctcctctg ccagccccac agccacagcc tggtgtatgt gtgcaagccg accttcgtgg 1020
ggagccgtga ccaagatggg gagatcctgc tgcccagaga ggtccccgat gagtatgaag 1080
ttggcagctt catggaggag gtgcgccagg agctggagga cctggagagg agcctgactg 1140
aagagatggc gctgggggag cctgcggctg ccgccgctgc actgctggga ggggaagaga 1200
tttagatctg gaccaggetg tgggtagatg tgcaatagaa atagetaatt tattteecca 1260
qqtqtqtqct ttaggcqtgq gctgaccagg cttcttccta catcttcttc ccagtaagtt 1320
tcccctctgg cttgacagca tgaggtgttg tgcatttgtt cagctccccc aggctgttct 1380
ccaggcttca cagtctggtg cttgggagag tcaggcaggg ttaaactgca ggagcagttt 1440
gccacccctg tccagattat tggctgcttt gcctctacca gttggcagac agccgtttgt 1500
tctacatggc tttgataatt gtttgagggg aggagatgga aacaatgtgg agtctccctc 1560
tqattqqttt tqqqqaaatq tqqaqaaqaq tgccctgctt tgcaaacatc aacctggcaa 1620
aaatgcaaca aatgaatttt ccacgcagtt ctttccatgg gcataggtaa gctgtgcctt 1680
cagctgttgc agatgaaatg ttctgttcac cctgcattac atgtgtttat tcatccagca 1740
gtgttgctca gctcctacct ctgtgccagg gcagcatttt catatccaag atcaattccc 1800
tctctcagca cagcctgggg agggggtcat tgttctcctc gtccatcagg gatctcagag 1860
gctcagagac tgcaagctgc ttgcccaagt cacacagcta gtgaagacca gagcagtttc 1920
atctggttgt gactctaagc tcagtgctct ctccactacc ccacaccagc cttggtgcca 1980
ccaaaagtgc tccccaaaag gaaggagaat gggatttttc ttgaggcatg cacatctgga 2040
attaaqqtca aactaattct cacatccctc taaaagtaaa ctactgttag gaacagcagt 2100
gttctcacag tgtggggcag ccgtccttct aatgaagaca atgatattga cactgtccct 2160
ctttggcagt tgcattagta actttgaaag gtatatgact gagcgtagca tacaggttaa 2220
cctqcagaaa cagtacttag gtaattgtag ggcgaggatt ataaatgaaa tttgcaaaat 2280
cacttagcag caactgaaga caattatcaa ccacgtggag aaaatcaaac cgagcagggc 2340
tgtgtgaaac atggttgtaa tatgcgactg cgaacactga actctacgcc actccacaaa 2400
tgatgttttc aggtgtcatg gactgttgcc accatgtatt catccagagt tcttaaagtt 2460
taaagttgca catgattgta taagcatgct ttctttgagt tttaaaattat gtataaacat 2520
aaqttqcatt taqaaatcaa qcataaatca cttcaactgc aaaaaaaaaa aaaaaaaaa 2580
                                                                  2586
aaaaaa
<210> 236
<211> 350
<212> PRT
<213> Homo sapiens
<400> 236
Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala
Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
```

40

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys

70

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn 85 90 95

Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His
100 105 110

Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
115 . 120 125

Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser 130 135 140

His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln 145 150 155 160

Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met 165 170 175

Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
180 185 190

Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys 195 200 205

Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg 210 215 220

Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu 225 230 235 240

Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu 245 250 255

Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu 260 265 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe 275 280 285

Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val 290 295 300

Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu 305 310 315 320

Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu
325 330 335

Pro Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile 340 345 350

<211> 17 <212> DNA	
<213> Artificial Sequence <220>	
<223> Synthetic oligonucleotide probe	
<400> 237 ggagctgcac cccttgc	17
<210> 238	
<211> 49	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic Oligonucleotide Probe	
<400> 238	
ggaggactgt gccaccatga gagactcttc aaacccaagg caaaattgg	49
<210> 239	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic Oligonucleotide Probe	
<400> 239	
gcagagegga gatgeagegg ettg	24
<210> 240	
<211> 18	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic Oligonucleotide Probe	
<400> 240	
ttggcagctt catggagg	18
<210> 241	
<211> 18	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic Oligonucleotide Probe	
<400> 241	
cctgggcaaa aatgcaac	18

```
<210> 242
<211> 24
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 242
                                                                    24
ctccagctcc tggcgcacct cctc
<210> 243
<211> 45
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 243
ggctctcagc taccgcgcag gagcgaggcc accctcaatg agatg
                                                                    45
<210> 244
<211> 3679
<212> DNA
<213> Homo Sapien
<400> 244
 aaggaggctg ggaggaaaga ggtaagaaag gttagagaac ctacctcaca 50
 tctctctggg ctcagaagga ctctgaagat aacaataatt tcagcccatc 100
 cacteteett ceeteecaaa cacacatgtg catgtacaca cacacataca 150
 cacacataca cetteetete etteactgaa gaeteacagt cacteaetet 200
 gtgagcaggt catagaaaag gaćactaaag cettaaggac aggeetggee 250
 attacctctg cagctccttt ggcttgttga gtcaaaaaac atgggagggg 300
 ccaggcacgg tgactcacac ctgtaatccc agcattttgg gagaccgagg 350
 tgagcagatc acttgaggtc aggagttcga gaccagcctg gccaacatgg 400
 agaaaccccc atctctacta aaaatacaaa aattagccag gagtggtggc 450
 aggtgcctgt aatcccagct actcaggtgg ctgagccagg agaatcgctt 500
 gaatccagga ggcggaggat gcagtcagct gagtgcaccg ctgcactcca 550
```

gcctgggtga cagaatgaga ctctgtctca aacaaacaaa cacgggagga 600

ggggtagata ctgcttctct gcaacctcct taactctgca tcctcttctt 650 ccagggctgc ccctgatggg gcctggcaat gactgagcag gcccagcccc 700 agaggacaag gaagagaagg catattgagg agggcaagaa gtgacgcccg 750 gtgtagaatg actgccctgg gagggtggtt ccttgggccc tggcagggtt 800 gctgaccctt accctgcaaa acacaaagag caggactcca gactctcctt 850 gtgaatggte ecctgeeetg cageteeace atgaggette tegtggeece 900 actcttgcta gcttgggtgg ctggtgccac tgccactgtg cccgtggtac 950 cctggcatgt tecctgeece ceteagtgtg cetgecagat ceggecetgg 1000 tatacgcccc gctcgtccta ccgcgaggct accactgtgg actgcaatga 1050 cctattcctg acggcagtcc ccccggcact ccccgcaggc acacagaccc 1100 tgctcctgca gagcaacagc attgtccgtg tggaccagag tgagctgggc 1150 tacctggcca atctcacaga gctggacctg tcccagaaca gcttttcgga 1200 tgcccgagac tgtgatttcc atgccctgcc ccagctgctg agcctgcacc 1250 tagaggagaa ccagctgacc cggctggagg accacagctt tgcagggctg 1300 gccagcctac aggaactcta tctcaaccac aaccagctct accgcatcgc 1350 ccccagggcc ttttctggcc tcagcaactt gctgcggctg cacctcaact 1400 ccaacctcct gagggccatt gacagccgct ggtttgaaat gctgcccaac 1450 ttggagatac tcatgattgg cggcaacaag gtagatgcca tcctggacat 1500 gaactteegg eeeetggeea acetgegtag eetggtgeta geaggeatga 1550 acctgcggga gatctccgac tatgccctgg aggggctgca aagcctggag 1600 agecteteet tetatgacaa eeagetggee egggtgeeea ggegggeaet 1650 ggaacaggtg cccgggctca agttcctaga cctcaacaag aacccgctcc 1700 agegggtagg geegggggae tttgccaaca tgctgcacct taaggagetg 1750 ggactgaaca acatggagga gctggtctcc atcgacaagt ttgccctggt 1800 gaacctcccc gagctgacca agctggacat caccaataac ccacggctgt 1850 ccttcatcca ccccgcgcc ttccaccacc tgccccagat ggagaccctc 1900 atgctcaaca acaacgctct cagtgccttg caccagcaga cggtggagtc 1950

cctgcccaac ctgcaggagg taggtctcca cggcaacccc atccgctgtg 2000 actgtgtcat ccgctgggcc aatgccacgg gcacccgtgt ccgcttcatc 2050 gageegeaat ceaecetgtg tgeggageet eeggacetee agegeeteee 2100 ggtccgtgag gtgcccttcc gggagatgac ggaccactgt ttgcccctca 2150 tetececacg aagetteece ceaageetee aggtageeag tggagagage 2200 atggtgctgc attgccgggc actggccgaa cccgaacccg agatctactg 2250 qqtcactcca gctgggcttc gactgacacc tgcccatgca ggcaggaggt 2300 accgggtgta ccccgagggg accctggagc tgcggagggt gacagcagaa 2350 gaggcagggc tatacacctg tgtggcccag aacctggtgg gggctgacac 2400 taagacggtt agtgtggttg tgggccgtgc tctcctccag ccaggcaggg 2450 acgaaggaca ggggctggag ctccgggtgc aggagaccca cccctatcac 2500 atcctgctat cttgggtcac cccacccaac acagtgtcca ccaacctcac 2550 ctggtccagt gcctcctccc tccggggcca gggggccaca gctctggccc 2600 gcctgcctcg gggaacccac agctacaaca ttacccgcct ccttcaggcc 2650 acggagtact gggcctgcct gcaagtggcc tttgctgatg cccacaccca 2700 gttggcttgt gtatgggcca ggaccaaaga ggccacttct tgccacagag 2750 ccttaqqqqa tcqtcctqqq ctcattqcca tcctqqctct cqctqtcctt 2800 ctcctggcag ctgggctagc ggcccacctt ggcacaggcc aacccaggaa 2850 gggtgtgggt gggaggcggc ctctccctcc agcctgggct ttctggggct 2900 ggagtgcccc ttctgtccgg gttgtgtctg ctcccctcgt cctgccctgg 2950 aatccaggga ggaagctgcc cagatcctca gaaggggaga cactgttgcc 3000 accattgtct caaaattctt gaagctcagc ctgttctcag cagtagagaa 3050 atcactagga ctacttttta ccaaaagaga agcagtctgg gccagatgcc 3100 ctgccaggaa agggacatgg acccacgtgc ttgaggcctg gcagctgggc 3150 caagacagat ggggctttgt ggccctgggg gtgcttctgc agccttgaaa 3200 aagttgccct tacctcctag ggtcacctct gctgccattc tgaggaacat 3250

ctccaaggaa caggaggac tttggctaga gcctcctgcc tccccatctt 3300 ctctctgccc agaggctcct gggcctggct tggctgtccc ctacctgtgt 3350 ccccgggctg caccccttcc tcttctcttt ctctgtacag tctcagttgc 3400 ttgctcttgt gcctcctggg caagggctga aggaggccac tccatctcac 3450 ctcggggggc tgccctcaat gtgggagtga ccccagccag atctgaagga 3500 catttgggag agggatgccc aggaacgcct catctcagca gcctgggctc 3550 ggcattccga agctgacttt ctataggcaa ttttgtacct ttgtggagaa 3600 atgtgtcacc tcccccaacc cgattcactc ttttctcctg ttttgtaaaa 3650 aataaaaata aataataaca ataaaaaaa 3679

<210> 245

<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

Met Arg Leu Leu Val Ala Pro Leu Leu Leu Ala Trp Val Ala Gly
1 5 10 15

Ala Thr Ala Thr Val Pro Val Val Pro Trp His Val Pro Cys Pro 20 25 30

Pro Gln Cys Ala Cys Gln Ile Arg Pro Trp Tyr Thr Pro Arg Ser 35 40 45

Ser Tyr Arg Glu Ala Thr Thr Val Asp Cys Asn Asp Leu Phe Leu
50 55 60

Thr Ala Val Pro Pro Ala Leu Pro Ala Gly Thr Gln Thr Leu Leu
65 70 75

Leu Gln Ser Asn Ser Ile Val Arg Val Asp Gln Ser Glu Leu Gly
80 85 90

Tyr Leu Ala Asn Leu Thr Glu Leu Asp Leu Ser Gln Asn Ser Phe 95 100 105

Ser Asp Ala Arg Asp Cys Asp Phe His Ala Leu Pro Gln Leu Leu 110 115 120

Ser Leu His Leu Glu Glu Asn Gln Leu Thr Arg Leu Glu Asp His
125 130 135

Ser Phe Ala Gly Leu Ala Ser Leu Gln Glu Leu Tyr Leu Asn His 140 145 150

Asn	Gln	Leu	Tyr	Arg 155	Ile	Ala	Pro	Arg	Ala 160	Phe	Ser	Gly	Leu	Ser 165
Asn	Leu	Leu	Arg	Leu 170	His	Leu	Asn	Ser	Asn 175	Leu	Leu	Arg	Ala	Ile 180
Asp	Ser	Arg	Trp	Phe 185	Glu	Met	Leu	Pro	Asn 190	Leu	Glu	Ile	Leu	Met 195
Ile	Gly	Gly	Asn	Lys 200	Val	Asp	Ala	Ile	Leu 205	Asp	Met	Asn	Phe	Arg 210
Pro	Leu	Ala	Asn	Leu 215	Arg	Ser	Leu	Val	Leu 220	Ala	Gly	Met	Asn	Leu 225
Arg	Glu	Ile	Ser	Asp 230	Tyr	Ala	Leu	Glu	Gly 235	Leu	Gln	Ser	Leu	Glu 240
Ser	Leu	Ser	Phe	Tyr 245	Asp	Asn	Gln	Leu	Ala 250	Arg	Val	Pro	Arg	Arg 255
Ala	Leu	Glu	Gln	Val 260	Pro	Gly	Leu	Lys	Phe 265	Leu	Asp	Leu	Asn	Lys 270
Asn	Pro	Leu	Gln	Arg 275	Val	Gly	Pro	Gly	Asp 280	Phe	Ala	Asn	Met	Leu 285
His	Leu	Lys	Glu	Leu 290	Gly	Leu	Asn	Asn	Met 295	Glu	Glu	Leu	Val	Ser 300
Ile	Asp	Lys	Phe	Ala 305	Leu	Val	Asn	Leu	Pro 310	Glu	Leu	Thr	Lys	Leu 315
Asp	Ile	Thr	Asn	Asn 320	Pro	Arg	Leu	Ser	Phe 325	Ile	His	Pro	Arg	Ala 330
Phe	His	His	Leu	Pro 335	Gln	Met	Glu	Thr	Leu 340	Met	Leu	Asn	Asn	Asn 345
Ala	Leu	Ser	Ala	Leu 350	His	Gln	Gln	Thr	Val 355	Glu	Ser	Leu	Pro	Asn 360
Leu	Gln	Glu	Val	Gly 365	Leu	His	Gly	Asn	Pro 370	Ile	Arg	Cys	Asp	Cys 375
Val	Ile	Arg	Trp	Ala 380	Asn	Ala	Thr	Gly	Thr 385	Arg	Val	Arg	Phe	Ile 390
Glu	Pro	Gln	Ser	Thr 395	Leu	Cys	Ala	Glu	Pro 400	Pro	Asp	Leu	Gln	Arg 405
Leu	Pro	Val	Arg	Glu	Val	Pro	Phe	Arg	Glu	Met	Thr	Asp	His	Cys

				410					415					420
Leu	Pro	Leu	Ile	Ser 425	Pro	Arg	Ser	Phe	Pro 430	Pro	Ser	Leu	Gln	Val 435
Ala	Ser	Gly	Glu	Ser 440	Met	Val	Leu	His	Cys 445	Arg	Ala	Leu	Ala	Glu 450
Pro	Glu	Pro	Glu	Ile 455	Tyr	Trp	Val	Thr	Pro 460	Ala	Gly	Leu	Arg	Leu 465
Thr	Pro	Ala	His	Ala 470	Gly	Arg	Arg	Tyr	Arg 475	Val	Tyr	Pro	Glu	Gly 480
Thr	Leu	Glu	Leu	Arg 485	Arg	Val	Thr	Ala	Glu 490	Glu	Ala	Gly	Leu	Tyr 495
Thr	Cys	Val	Ala	Gln 500	Asn	Leu	Val	Gly	Ala 505	Asp	Thr	Lys	Thr	Val 510
Ser	Val	Val	Val	Gly 515	Arg	Ala	Leu	Leu	Gln 520	Pro	Gly	Arg	Asp	Glu 525
Gly	Gln	Gly	Leu	Glu 530	Leu	Arg	Val	Gln	Glu 535	Thr	His	Pro	Tyr	His 540
Ile	Leu	Leu	Ser	Trp 545	Val	Thr	Pro	Pro	Asn 550	Thr	Val	Ser	Thr	Asn 555
Leu	Thr	Trp	Ser	Ser 560	Ala	Ser	Ser	Leu	Arg 565	Gly	Gln	Gly	Ala	Thr 570
Ala	Leu	Ala	Arg	Leu 575	Pro	Arg	Gly	Thr	His 580	Ser	Tyr	Asn	Ile	Thr 585
Arg	Leu	Leu	Gln	Ala 590	Thr	Glu	Tyr	Trp	Ala 595	Cys	Leu	Gln	Val	Ala 600
Phe	Ala	Asp	Ala	His 605	Thr	Gln	Leu	Ala	Cys 610	Val	Trp	Ala	Arg	Thr 615
Lys	Glu	Ala	Thr	Ser 620	Cys	His	Arg	Ala	Leu 625	Gly	Asp	Arg	Pro	Gly 630
Leu	Ile	Ala	Ile	Leu 635	Ala	Leu	Ala	Val	Leu 640	Leu	Leu	Ala	Ala	Gly 645
Leu	Ala	Ala	His	Leu 650	Gly	Thr	Gly	Gln	Pro 655	Arg	Lys	Gly	Val	Gly 660
Gly	Arg	Arg	Pro	Leu 665	Pro	Pro	Ala	Trp	Ala 670	Phe	Trp	Gly	Trp	Ser 675

```
Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp
                   680
                                        685
                                                            690
   Asn Pro Gly Arg Lys Leu Pro Arg Ser Ser Glu Gly Glu Thr Leu
                   695
                                        700
   Leu Pro Pro Leu Ser Gln Asn Ser
                   710
  <210> 246
  <211> 22
  <212> DNA
  <213> Artificial Sequence
  <220>
  <223> Synthetic Oligonucleotide Probe
  <400> 246
   aacaaggtaa gatgccatcc tg 22
. <210> 247
  <211> 24
  <212> DNA
  <213> Artificial Sequence
  <220>
  <223> Synthetic Oligonucleotide Probe
  <400> 247
  aaacttgtcg atggagacca gctc 24
  <210> 248
  <211> 45
  <212> DNA
  <213> Artificial Sequence
  <223> Synthetic Oligonucleotide Probe
  <400> 248
   aggggctgca aagcctggag agcctctcct tctatgacaa ccagc 45
  <210> 249
  <211> 3401
  <212> DNA
  <213> Homo Sapien
   gcaagccaag gcgctgtttg agaaggtgaa gaagttccgg acccatgtgg 50
   aggagggga cattgtgtac cgcctctaca tgcggcagac catcatcaag 100
```

gtgatcaagt tcatcctcat catctgctac accgtctact acgtgcacaa 150

catcaagttc gacgtggact gcaccgtgga cattgagagc ctgacgggct 200 accgcaccta ccgctgtgcc caccccttgg ccacactctt caagatcctg 250 gcgtccttct acatcagcct agtcatcttc tacggcctca tctgcatgta 300 cacactgtgg tggatgctac ggcgctccct caagaagtac tcgtttgagt 350 cgatccgtga ggagagcagc tacagcgaca tccccgacgt caagaacgac 400 ttcgccttca tgctgcacct cattgaccaa tacgacccgc tctactccaa 450 gcgcttcgcc gtcttcctgt cggaggtgag tgagaacaag ctgcggcagc 500 tgaacctcaa caacgagtgg acgctggaca agctccggca gcggctcacc 550 aagaacgcgc aggacaagct ggagctgcac ctgttcatgc tcagtggcat 600 ccctgacact gtgtttgacc tggtggagct ggaggtcctc aagctggagc 650 tgatccccga cgtgaccatc ccgcccagca ttgcccagct cacgggcctc 700 aaggagetgt ggetetaeea cacageggee aagattgaag egeetgeget 750 ggccttcctg cgcgagaacc tgcgggcgct gcacatcaag ttcaccgaca 800 tcaaggagat cccgctgtgg atctatagcc tgaagacact ggaggagctg 850 cacctgacgg gcaacctgag cgcggagaac aaccgctaca tcgtcatcga 900 cgggctgcgg gagctcaaac gcctcaaggt gctgcggctc aagagcaacc 950 taagcaagct gccacaggtg gtcacagatg tgggcgtgca cctgcagaag 1000 ctgtccatca acaatgaggg caccaagctc atcgtcctca acagcctcaa 1050 gaagatggcg aacctgactg agctggagct gatccgctgc gacctggagc 1100 gcatececea etecatette ageeteeaca acetgeagga gattgacete 1150 aaggacaaca acctcaagac catcgaggag atcatcagct tccagcacct 1200 gcaccgcctc acctgcctta agctgtggta caaccacatc gcctacatcc 1250 ccatccagat cggcaacctc accaacctgg agcgcctcta cctgaaccgc 1300 aacaagateg agaagateee cacceagete ttetaetgee geaagetgeg 1350 ctacctggac ctcagccaca acaacctgac cttcctccct gccgacatcg 1400 geeteetgea gaaceteeag aacetageea teaeggeeaa eeggategag 1450

acgctccctc cggagctctt ccagtgccgg aagctgcggg ccctgcacct 1500 gggcaacaac gtgctgcagt cactgccctc cagggtgggc gagctgacca 1550 acctgacgca gatcgagctg cggggcaacc ggctggagtg cctgcctgtg 1600 gagetgggeg agtgeecaet geteaagege ageggettgg tggtggagga 1650 ggacctgttc aacacactgc cacccgaggt gaaggagcgg ctgtggaggg 1700 ctgacaagga gcaggcctga gcgaggccgg cccagcacag caagcagcag 1750 gaccgctgcc cagtcctcag gcccggaggg gcaggcctag cttctcccag 1800 aactcccgga cagccaggac agcctcgcgg ctgggcagga gcctggggcc 1850 gcttgtgagt caggccagag cgagaggaca gtatctgtgg ggctggcccc 1900 ttttctccct ctgagactca cgtcccccag ggcaagtgct tgtggaggag 1950 agcaagtete aagagegeag tatttggata atcagggtet cetecetgga 2000 ggccagctct gccccagggg ctgagctgcc accagaggtc ctgggaccct 2050 cactttagtt cttggtattt atttttctcc atctcccacc tccttcatcc 2100 agataactta tacattccca agaaagttca gcccagatgg aaggtgttca 2150 gggaaaggtg ggctgccttt tccccttgtc cttatttagc gatgccgccg 2200 ggcatttaac acccacctgg acttcagcag agtggtccgg ggcgaaccag 2250 ccatgggacg gtcacccagc agtgccgggc tgggctctgc ggtgcggtcc 2300 acgggagagc aggcctccag ctggaaaggc caggcctgga gcttgcctct 2350 tcagtttttg tggcagtttt agttttttgt ttttttttt tttaatcaaa 2400 aaacaatttt ttttaaaaaa aagctttgaa aatggatggt ttgggtatta 2450 aaaagaaaaa aaaaacttaa aaaaaaaaag acactaacgg ccagtgagtt 2500 ggagtctcag ggcagggtgg cagtttccct tgagcaaagc agccagacgt 2550 tgaactgtgt ttcctttccc tgggcgcagg gtgcagggtg tcttccggat 2600 ctggtgtgac cttggtccag gagttctatt tgttcctggg gagggaggtt 2650 tttttgtttg ttttttgggt ttttttggtg tcttgttttc tttctcctcc 2700 atgtgtettg geaggeacte atttetgtgg etgteggeea gagggaatgt 2750 tetggagetg ceaaggaggg aggagaeteg ggttggetaa tecceggatg 2800

aacggtgete cattegcace tecectecte gtgeetgeee tgeeteteea 2850 egeacagtgt taaggageea agaggageea ettegeeeag actttgttte 2900 eeeaceteet geggeatggg tgtgteeagt geeacegetg geeteegetg 2950 ettecateag eeetgtegee acetggteet teatgaagag cagacactta 3000 gaggetggte gggaatgggg aggtegeee tgggaaggea ggegttggtt 3050 eeaageeggt teeegteeet ggegeetgga gtgeacacag eeeagtegge 3100 acetggtgge tggaageeaa eetgetttag ateacteggg teeecacett 3150 agaagggtee eegeettaga teaateaegt ggacactaag geacgtttta 3200 gagtetettg tettaatgat tatgteeate egtetgteeg teeatttgtg 3250 ttttetgegt egtgteattg gatataatee teagaaataa tgeacactag 3300 eetetgacaa eeatgaagea aaaateegtt acatgtgggt etgaacttgt 3350 agaeteggte acagtateaa ataaaateta taacagaaaa aaaaaaaaaa 3400 a 3401

<210> 250

<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

Met Arg Gln Thr Ile Ile Lys Val Ile Lys Phe Ile Leu Ile Ile 1 5 10 15

Cys Tyr Thr Val Tyr Tyr Val His Asn Ile Lys Phe Asp Val Asp 20 25 30

Cys Thr Val Asp Ile Glu Ser Leu Thr Gly Tyr Arg Thr Tyr Arg 35 40 45

Cys Ala His Pro Leu Ala Thr Leu Phe Lys Ile Leu Ala Ser Phe
50 55 60

Tyr Ile Ser Leu Val Ile Phe Tyr Gly Leu Ile Cys Met Tyr Thr
65 70 75

Leu Trp Trp Met Leu Arg Arg Ser Leu Lys Lys Tyr Ser Phe Glu 80 85 90

Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile Pro Asp Val Lys

				95					100					105
Asn .	Asp	Phe	Ala	Phe 110	Met	Leu	His	Leu	Ile 115	Asp	Gln	Tyr	Asp	Pro 120
Leu	Tyr	Ser	Lys	Arg 125	Phe	Ala	Val	Phe	Leu 130	Ser	Glu	Val	Ser	Glu 135
Asn	Lys	Leu	Arg	Gln 140	Leu	Asn	Leu	Asn	Asn 145	Glu	Trp	Thr	Leu	Asp 150
Lys	Leu	Arg	Gln	Arg 155	Leu	Thr	Lys	Asn	Ala 160	Gln	Asp	Lys	Leu	Glu 165
Leu	His	Leu	Phe	Met 170	Leu	Ser	Gly	Ile	Pro 175	Asp	Thr	Val	Phe	Asp 180
Leu	Val	Glu	Leu	Glu 185	Val	Leu	Lys	Leu	Glu 190	Leu	Ile	Pro	Asp	Val 195
Thr	Ile	Pro	Pro	Ser 200	Ile	Ala	Gln	Leu	Thr 205	Gly	Leu	Lys	Glu	Leu 210
Trp	Leu	Tyr	His	Thr 215	Ala	Ala	Lys	Ile	Glu 220	Ala	Pro	Ala	Leu	Ala 225
Phe	Leu	Arg	Glu	Asn 230	Leu	Arg	Ala	Leu	His 235	Ile	Lys	Phe	Thr	Asp 240
Ile	Lys	Glu	Ile	Pro 2 4 5	Leu	Trp	Ile	Tyr	Ser 250	Leu	Lys	Thr	Leu	Glu 255
Glu	Leu	His	Leu	Thr 260	Gly	Asn	Leu	Ser	Ala 265	Glu	Asn	Asn	Arg	Tyr 270
Ile	Val	Ile	Asp	Gly 275	Leu	Arg	Glu	Leu	Lys 280	Arg	Leu	Lys	Val	Leu 285
Arg	Leu	Lys	Ser	Asn	Leu	Ser	Lys	Leu	Pro	Gln	Val	Val	Thr	Asp
				290					295					300
Val	Gly	Val	His	Leu 305	Gln	Lys	Leu	Ser	Ile 310	Asn	Asn	Glu	Gly	Thr 315
Lys	Leu	Ile	Val	Leu 320	Asn	Ser	Leu	Lys	Lys 325	Met	Ala	Asn	Leu	Thr 330
Glu	Leu	Glu	Leu	11e 335	Arg	Суѕ	Asp	Leu	Glu 340	Arg	Ile	Pro	His	Ser 345
Ile	Phe	Ser	Leu	His	Asn	Leu	Gln	Glu	Ile 355	Asp	Leu	Lys	Asp	Asn 360

<210> 252 <211> 24

Asn Leu Lys Thr Ile Glu Glu Ile Ile Ser Phe Gln His Leu His 370 Arg Leu Thr Cys Leu Lys Leu Trp Tyr Asn His Ile Ala Tyr Ile 380 Pro Ile Gln Ile Gly Asn Leu Thr Asn Leu Glu Arg Leu Tyr Leu 400 405 395 Asn Arq Asn Lys Ile Glu Lys Ile Pro Thr Gln Leu Phe Tyr Cys 415 410 Arg Lys Leu Arg Tyr Leu Asp Leu Ser His Asn Asn Leu Thr Phe 425 Leu Pro Ala Asp Ile Gly Leu Leu Gln Asn Leu Gln Asn Leu Ala Ile Thr Ala Asn Arg Ile Glu Thr Leu Pro Pro Glu Leu Phe Gln Cys Arg Lys Leu Arg Ala Leu His Leu Gly Asn Asn Val Leu Gln 475 470 Ser Leu Pro Ser Arg Val Gly Glu Leu Thr Asn Leu Thr Gln Ile Glu Leu Arg Gly Asn Arg Leu Glu Cys Leu Pro Val Glu Leu Gly 505 Glu Cys Pro Leu Leu Lys Arg Ser Gly Leu Val Val Glu Glu Asp 520 515 Leu Phe Asn Thr Leu Pro Pro Glu Val Lys Glu Arg Leu Trp Arg Ala Asp Lys Glu Gln Ala 545 <210> 251 <211> 20 <212> DNA <213> Artificial Sequence <223> Synthetic Oligonucleotide Probe <400> 251 caacaatgag ggcaccaagc 20

```
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 252
gatggctagg ttctggaggt tctg 24
<210> 253
<211> 47
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 253
caacctgcag gagattgacc tcaaggacaa caacctcaag accatcg 47
<210> 254
<211> 1650
<212> DNA
<213> Homo Sapien
<400> 254
 gcctgttgct gatgctgccg tgcggtactt gtcatggagc tggcactgcg 50
 gegetetece gteeegeggt ggttgetget getgeegetg etgetgggee 100
 tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150
 tgggattatg tgacggtccg caaggatgcc tacatgttct ggtggctcta 200
 ttatgccacc aactcctgca agaacttctc agaactgccc ctggtcatgt 250
 ggcttcaggg cggtccaggc ggttctagca ctggatttgg aaactttgag 300
 gaaattgggc cccttgacag tgatctcaaa ccacggaaaa ccacctggct 350
 ccaggetgec agtetectat ttgtggataa teeegtggge aetgggttea 400
 gttatgtgaa tggtagtggt gcctatgcca aggacctggc tatggtggct 450
 tcagacatga tggttctcct gaagaccttc ttcagttgcc acaaagaatt 500
 ccagacagtt ccattctaca ttttctcaga gtcctatgga ggaaaaatgg 550
 cagctggcat tggtctagag ctttataagg ccattcagcg agggaccatc 600
 aagtgcaact ttgcgggggt tgccttgggt gattcctgga tctcccctgt 650
 tgattcggtg ctctcctggg gaccttacct gtacagcatg tctcttctcg 700
```

aaqacaaagg tctggcagag gtgtctaagg ttgcagagca agtactgaat 750 gccgtaaata aggggctcta cagagaggcc acagagctgt gggggaaagc 800 agaaatqatc attqaacaga acacagatgg ggtgaacttc tataacatct 850 taactaaaag cactcccacg tctacaatgg agtcgagtct agaattcaca 900 cagagecace tagtttgtct ttgtcagege caegtgagae acctacaaeg 950 agatgcctta agccagctca tgaatggccc catcagaaag aagctcaaaa 1000 ttattcctqa qgatcaatcc tggggaggcc aggctaccaa cgtctttgtg 1050 aacatggagg aggacttcat gaagccagtc attagcattg tggacgagtt 1100 gctggaggca gggatcaacg tgacggtgta taatggacag ctggatctca 1150 tcqtaqatac catgggtcag gaggcctggg tgcggaaact gaagtggcca 1200 gaactgccta aattcagtca gctgaagtgg aaggccctgt acagtgaccc 1250 taaatctttg gaaacatctg cttttgtcaa gtcctacaag aaccttgctt 1300 tctactggat tctgaaagct ggtcatatgg ttccttctga ccaaggggac 1350 atggctctga agatgatgag actggtgact cagcaagaat aggatggatg 1400 qqqctqqaqa tgagctggtt tggccttggg gcacagagct gagctgaggc 1450 cqctgaagct gtaggaagcg ccattettee ctgtatetaa ctggggctgt 1500 gatcaagaag gttctgacca gcttctgcag aggataaaat cattgtctct 1550 ggaggcaatt tggaaattat ttctgcttct taaaaaaacc taagattttt 1600 taaaaaattq atttqttttq atcaaaataa aggatgataa tagatattaa 1650

<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

Met Glu Leu Ala Leu Arg Arg Ser Pro Val Pro Arg Trp Leu Leu 1 5 10 15

Leu Leu Pro Leu Leu Gly Leu Asn Ala Gly Ala Val Ile Asp
20 25 30

Trp Pro Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val

Arg	Lys	Asp	Ala	Tyr 50	Met	Phe	Trp	Trp	Leu 55	Tyr	Tyr	Ala	Thr	Asn 60
Ser	Cys	Lys	Asn	Phe 65	Ser	Glu	Leu	Pro	Leu 70	Val	Met	Trp	Leu	Gln 75
Gly	Gly	Pro	Gly	Gly 80	Ser	Ser	Thr	Gly	Phe 85	Gly	Asn	Phe	Glu	Glu 90
Ile	Gly	Pro	Leu	Asp 95	Ser	Asp	Leu	Lys	Pro 100	Arg	Lys	Thr	Thr	Trp 105
Leu	Gln	Ala	Ala	Ser 110	Leu	Leu	Phe	Val	Asp 115	Asn	Pro	Val	Gly	Thr 120
Gly	Phe	Ser	Tyr	Val 125	Asn	Gly	Ser	Gly	Ala 130	Tyr	Ala	Lys	Asp	Leu 135
Ala	Met	Val	Ala	Ser 140	Asp	Met	Met	Val	Leu 145	Leu	Lys	Thr	Phe	Phe 150
Ser	Cys	His	Lys	Glu 155	Phe	Gln	Thr	Val	Pro 160	Phe	Tyr	Ile	Phe	Ser 165
Glu	Ser	Tyr	Gly	Gly 170	Lys	Met	Ala	Ala	Gly 175	Ile	Gly	Leu	Glu	Leu 180
Tyr	Lys	Ala	Ile	Gln 185	Arg	Gly	Thr	Ile	Lys 190	Cys	Asn	Phe	Ala	Gly 195
Val	Ala	Leu	Gly	Asp 200	Ser	Trp	Ile	Ser	Pro 205	Val	Asp	Ser	Val	Leu 210
Ser	Trp	Gly	Pro	Tyr 215	Leu	Tyr	Ser	Met	Ser 220	Leu	Leu	Glu	Asp	Lys 225
Gly	Leu	Ala	Glu	Val 230	Ser	Lys	Val	Ala	Glu 235	Gln	Val	Leu	Asn	Ala 240
Val	Asn	Lys	Gly	Leu 245	Tyr	Arg	Glu	Ala	Thr 250	Glu	Leu	Trp	Gly	Lys 255
Ala	Glu	Met	Ile	Ile 260	Glu	Gln	Asn	Thr	Asp 265	Gly	Val	Asn	Phe	Tyr 270
Asn	Ile	Leu	Thr	Lys 275	Ser	Thr	Pro	Thr	Ser 280	Thr	Met	Glu	Ser	Ser 285
Leu	Glu	Phe	Thr	Gln 290	Ser	His	Leu	Val	Cys 295	Leu	Cys	Gln	Arg	His 300
Val	Arg	His	Leu	Gln	Arg	Asp	Ala	Leu	Ser	Gln	Leu	Met	Asn	Gly

				305					310					315
Pro	Ile	Arg	Lys	Lys 320	Leu	Lys	Ile	Ile	Pro 325	Glu	Asp	Gln	Ser	Trp 330
Gly	Gly	Gln	Ala	Thr 335	Asn	Val	Phe	Val	Asn 340	Met	Glu	Glu	Asp	Phe 345
Met	Lys	Pro	Val	Ile 350	Ser	Ile	Val	Asp	Glu 355	Leu	Leu	Glu	Ala	Gly 360
Ile	Asn	Val	Thr	Val 365	Tyr	Asn	Gly	Gln	Leu 370	Asp	Leu	Ile	Val	Asp 375
Thr	Met	Gly	Gln	Glu 380	Ala	Trp	Val	Arg	Lys 385	Leu	Lys	Trp	Pro	Glu 390
Leu	Pro	Lys	Phe	Ser 395	Gln	Leu	Lys	Trp	Lys 400	Ala	Leu	Tyr	Ser	Asp 405
Pro	Lys	Ser	Leu	Glu 410	Thr	Ser	Ala	Phe	Val 415	Lys	Ser	Tyr	Lys	Asn 420
Leu	Ala	Phe	Туr	Trp 425	Ile	Leu	Lys	Ala	Gly 430	His	Met	Val	Pro	Ser 435
Asp	Gln	Gly	Asp	Met 440	Ala	Leu	Lys	Met	Met 445	Arg	Leu	Val	Thr	Gln 450
Gln	Glu													

<210> 256

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

ggccgcgga gaggaggca tgggcgcg cggggcgctg ctgctggcg 50
tgctgctggc tcgggctgga ctcaggaagc cggagtcgca ggaggcggcg 100
ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcatcgtggg 150
tggagaggac gccgaactcg ggcgttggcc gtggcagggg agcctgcgcc 200
tgtgggattc ccacgtatgc ggagtgagcc tgctcagcca ccgctgggca 250
ctcacggcgg cgcactgctt tgaaacctat agtgacctta gtgatccctc 300
cgggtggatg gtccagtttg gccagctgac ttccatgcca tccttctgga 350
gcctgcaggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400

tgcacctgtc acctacacta accatacta gcccatctgt ctccaggcct 500 ccacatttga gtttgagaac cggacagact gctgggtgac tggctggggg 550 tacatcaaag aggatgaggc actgccatct ccccacaccc tccaggaagt 600 tcaggtcgcc atcataaaca actctatgtg caaccacctc ttcctaagt 650 acagtttccg caaggacatc tttggagaca tggtttgtgc tggcaacgcc 700 caaggcggga aggatgcctg cttcggtgac tcaggtggac ccttggcctg 750 taacaagaat ggactgtgt atcagattg agtcgtgac tcaggtggac ccttggcctg 750 taacaagaat ggactgtgt atcagattg agtcgtgac tggggagtgg 800 gctgtggtc gcccaatcgg cccggtgtct acaccaatat cagccaccac 850 tttgagtgac tcagaagct gatggccag agtggcatg cccacacacc 500 cccctcctgg ccactactct ttttccctct tctctggct ctcccactcc 950 tgggggccggt ctgagcctac ctgagcccat gcagccaga agacctggg gccactgcca 1000 agtcaggccc tggttcttc tctcaaaaaa aaaaaaaaa cacaatccaa 1050 ttgatgtcgt gcaggccatt cttcaaaaaa aaaaaaaaa aaaaaaaaa 1100

<400> 257

Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg
1 5 10 15

Ala Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser

20 25 30

Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly 35 40 45

Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg
50 55 60

Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg
65 70 75

Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr Ser Asp Leu 80 85 90

<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

```
Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser
                                                         105
                 95
                                     100
Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe
                110
                                     115
Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro
                                     130
                125
Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr
Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe
                155
Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys
                170
                                                          180
Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln
Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys
Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly
                215
Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly
Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val
                                     250
                245
Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val
Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met
                275
Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu
                                                          300
                 290
                                     295
Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val
                 305
                                     310
```

<210> 258

<211> 2427

<212> DNA

<213> Homo Sapien

<400> 258

cccacgcgtc cgcggacgcg tgggaagggc agaatgggac tccaagcctg 50

cctcctaggg ctctttgccc tcatcctctc tggcaaatgc agttacagcc 100 cggagcccga ccagcggagg acgctgccc caggctgggt gtccctgggc 150 cgtgcggacc ctgaggaaga gctgagtctc acctttgccc tgagacagca 200 qaatgtggaa agactctcgg agctggtgca ggctgtgtcg gatcccagct 250 ctcctcaata cggaaaatac ctgaccctag agaatgtggc tgatctggtg 300 aggecatece caetgaceet ceaeaeggtg caaaaatgge tettggeage 350 cggagcccag aagtgccatt ctgtgatcac acaggacttt ctgacttgct 400 ggctgagcat ccgacaagca gagctgctgc tccctggggc tgagtttcat 450 cactatgtgg gaggacetae ggaaacecat gttgtaaggt ceceacatee 500 ctaccagett ccacaggeet tggcccccca tgtggaettt gtggggggac 550 tgcaccgttt tcccccaaca tcatccctga ggcaacgtcc tgagccgcag 600 gtgacaggga ctgtaggcct gcatctgggg gtaaccccct ctgtgatccg 650 taagcgatac aacttgacct cacaagacgt gggctctggc accagcaata 700 acagccaagc ctgtgcccag ttcctggagc agtatttcca tgactcagac 750 ctggctcagt tcatgcgcct cttcggtggc aactttgcac atcaggcatc 800 ccaqtctaga tgtgcagtac ctgatgagtg ctggtgccaa catctccacc 900 tgggtctaca gtagccctgg ccggcatgag ggacaggagc ccttcctgca 950 gtggctcatg ctgctcagta atgagtcagc cctgccacat gtgcatactg 1000 tgagetatgg agatgatgag gaeteeetea geagegeeta eateeagegg 1050 gtcaacactg agctcatgaa ggctgccgct cggggtctca ccctgctctt 1100 cgcctcaggt gacagtgggg ccgggtgttg gtctgtctct ggaagacacc 1150 agttccgccc taccttccct gcctccagcc cctatgtcac cacagtggga 1200 ggcacatcct tccaggaacc tttcctcatc acaaatgaaa ttgttgacta 1250 tatcagtggt ggtggcttca gcaatgtgtt cccacggcct tcataccagg 1300 aggaagetgt aacgaagtte etgageteta geeceeacet geeaceatee 1350 agttacttca atgccagtgg ccgtgcctac ccagatgtgg ctgcactttc 1400

tgatggctac tgggtggtca gcaacagagt gcccattcca tgggtgtccg 1450 gaacctcggc ctctactcca gtgtttgggg ggatcctatc cttgatcaat 1500 gagcacagga tccttagtgg ccgccccct cttggctttc tcaacccaag 1550 gctctaccag cagcatgggg caggtctctt tgatgtaacc cgtggctgcc 1600 atgagtcctg tctggatgaa gaggtagagg gccagggttt ctgctctggt 1650 cctggctggg atcctgtaac aggctgggga acaccaactt cccagctttg 1700 ctgaagactc tactcaaccc ctgacccttt cctatcagga gagatggctt 1750 gtcccctgcc ctgaagctgg cagttcagtc ccttattctg ccctgttgga 1800 agecetgetg aaccetcaac tattgactge tgeagacage ttateteeet 1850 aaccetgaaa tgetgtgage ttgaettgae teecaaceet accatgetee 1900 atcatactca ggtctcccta ctcctgcctt agattcctca ataagatgct 1950 gtaactagca ttttttgaat gcctctccct ccgcatctca tctttctctt 2000 ttcaatcagg cttttccaaa gggttgtata cagactctgt gcactatttc 2050 acttgatatt cattccccaa ttcactgcaa ggagacctct actgtcaccg 2100 tttactcttt cctaccctga catccagaaa caatggcctc cagtgcatac 2150 ttctcaatct ttgctttatg gcctttccat catagttgcc cactccctct 2200 cettacttag ettecaggie ttaacttete tgaetactet tgtetteete 2250 tctcatcaat ttctgcttct tcatggaatg ctgaccttca ttgctccatt 2300 tgtagatttt tgctcttctc agtttactca ttgtcccctg gaacaaatca 2350 ctgacatcta caaccattac catctcacta aataagactt tctatccaat 2400 aatgattgat acctcaaatg taaaaaa 2427

Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr

<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

Met Gly Leu Gln Ala Cys Leu Leu Gly Leu Phe Ala Leu Ile Leu
1 10 15

				20					25					30
Leu	Pro	Pro	Gly	Trp 35	Val	Ser	Leu	Gly	Arg 40	Ala	Asp	Pro	Glu	Glu 45
Glu	Leu	Ser	Leu	Thr 50	Phe	Ala	Leu	Arg	Gln 55	Gln	Asn	Val	Glu	Arg 60
Leu	Ser	Glu	Leu	Val 65	Gln	Ala	Val	Ser	Asp 70	Pro	Ser	Ser	Pro	Gln 75
Tyr	Gly	Lys	Tyr	Leu 80	Thr	Leu	Glu	Asn	Val 85	Ala	Asp	Leu	Val	Arg 90
Pro	Ser	Pro	Leu	Thr 95	Leu	His	Thr	Val	Gln 100	Lys	Trp	Leu	Leu	Ala 105
Ala	Gly	Ala	Gln	Lys 110	Cys	His	Ser	Val	Ile 115	Thr	Gln	Asp	Phe	Leu 120
Thr	Cys	Trp	Leu	Ser 125	Ile	Arg	Gln	Ala	Glu 130	Leu	Leu	Leu	Pro	Gly 135
Ala	Glu	Phe	His	His 140	Tyr	Val	Gly	Gly	Pro 145	Thr	Glu	Thr	His	Val 150
Val	Arg	Ser	Pro	His 155	Pro	Tyr	Gln	Leu	Pro 160	Gln	Ala	Leu	Ala	Pro
His	Val	Asp	Phe	Val 170	Gly	Gly	Leu	His	Arg 175	Phe	Pro	Pro	Thr	Ser 180
Ser	Leu	Arg	Gln	Arg 185	Pro	Glu	Pro	Gln	Val 190	Thr	Gly	Thr	Val	Gly 195
Leu	His	Leu	Gly	Val 200	Thr	Pro	Ser	Val	Ile 205	Arg	Lys	Arg	Tyr	Asn 210
Leu	Thr	Ser	Gln	Asp 215		Gly	Ser	Gly	Thr 220		Asn	Asn	Ser	Gln 225
Ala	Cys	Ala	Gln	Phe 230	Leu	Glu	Gln	Tyr	Phe 235	His	Asp	Ser	Asp	Leu 240
Ala	Gln	Phe	Met	Arg 245	Leu	Phe	Gly	Gly	Asn 250	Phe	Ala	His	Gln	Ala 255
Ser	Val	Ala	Arg	Val 260	Val	Gly	Gln	Gln	Gly 265	Arg	Gly	Arg	Ala	Gly 270
Ile	Glu	Ala	Ser	Leu	Asp	Val	Gln	Tyr	Leu	Met	Ser	Ala	Gly	Ala

Asn	Ile	Ser	Thr	Trp 290	Val	Tyr	Ser	Ser	Pro 295	Gly	Arg	His	Glu	Gly 300
Gln	Glu	Pro	Phe	Leu 305	Gln	Trp	Leu	Met	Leu 310	Leu	Ser	Asn	Glu	Ser 315
Ala	Leu	Pro	His	Val 320	His	Thr	Val	Ser	Tyr 325	Gly	Asp	Asp	Glu	Asp 330
Ser	Leu	Ser	Ser	Ala 335	Tyr	Ile	Gln	Arg	Val 340	Asn	Thr	Glu	Leu	Met 345
Lys	Ala	Ala	Ala	Arg 350	Gly	Leu	Thr	Leu	Leu 355	Phe	Ala	Ser	Gly	Asp 360
Ser	Gly	Ala	Gly	Cys 365	Trp	Ser	Val	Ser	Gly 370	Arg	His	Gln	Phe	Arg 375
Pro	Thr	Phe	Pro	Ala 380	Ser	Ser	Pro	Tyr	Val 385	Thr	Thr	Val	Gly	Gly 390
Thr	Ser	Phe	Gln	Glu 395	Pro	Phe	Leu	Ile	Thr 400	Asn	Glu	Ile	Val	Asp 405
Tyr	Ile	Ser	Gly	Gly 410	Gly	Phe	Ser	Asn	Val 415	Phe	Pro	Arg	Pro	Ser 420
Tyr	Gln	Glu	Glu	Ala 425	Val	Thr	Lys	Phe	Leu 430	Ser	Ser	Ser	Pro	His 435
Leu	Pro	Pro	Ser	Ser 440	Tyr	Phe	Asn	Ala	Ser 445	Gly	Arg	Ala	Tyr	Pro 450
Asp	Val	Ala	Ala	Leu 455	Ser	Asp	Gly	Tyr	Trp 460	Val	Val	Ser	Asn	Arg 465
Val	Pro	Ile	Pro	Trp 470	Val	Ser	Gly	Thr	Ser 47 5	Ala	Ser	Thr	Pro	Val 480
Phe	Gly	Gly	Ile	Leu 485	Ser	Leu	Ile	Asn	Glu 490	His	Arg	Ile	Leu	Ser 495
Gly	Arg	Pro	Pro	Leu 500	Gly	Phe	Leu	Asn	Pro 505	Arg	Leu	Tyr	Gln	Gln 510
His	Gly	Ala	Gly	Leu 515	Phe	Asp	Val	Thr	Arg 520	Gly	Cys	His	Glu	Ser 525
Cys	Leu	Asp	Glu	Glu 530	Val	Glu	Gly	Gln	Gly 535	Phe	Cys	Ser	Gly	Pro 540
Gly	Trp	Asp	Pro	Val 545	Thr	Gly	Trp	Gly	Thr 550	Pro	Thr	Ser	Gln	Leu 555

Cys

<210> 260 <211> 1638 <212> DNA

<213> Homo Sapien

<400> 260 geogegeget etetecegge geceacacet gtetgagegg egeagegage 50 egeggeeegg gegggetget eggegggaa eagtgetegg catggeaggg 100 attecaggge teetetteet tetettett etgetetgtg etgttgggea 150 agtgageeet tacagtgeee eetggaaace eacttggeet geataeegee 200 tccctgtcgt cttgccccag tctaccctca atttagccaa gccagacttt 250 ggagccgaag ccaaattaga agtatcttct tcatgtggac cccagtgtca 300 taagggaact ccactgccca cttacgaaga ggccaagcaa tatctgtctt 350 atgaaacgct ctatgccaat ggcagccgca cagagacgca ggtgggcatc 400 tacatcctca gcagtagtgg agatggggcc caacaccgag actcagggtc 450 ttcaggaaag tctcgaagga agcggcagat ttatggctat gacagcaggt 500 tcagcatttt tgggaaggac ttcctgctca actacccttt ctcaacatca 550 gtgaagttat ccacgggctg caccggcacc ctggtggcag agaagcatgt 600 cctcacagct gcccactgca tacacgatgg aaaaacctat gtgaaaggaa 650 cccagaagct tcgagtgggc ttcctaaagc ccaagtttaa agatggtggt 700 cgaggggcca acgactccac ttcagccatg cccgagcaga tgaaatttca 750 gtggatccgg gtgaaacgca cccatgtgcc caagggttgg atcaagggca 800 atgccaatga catcggcatg gattatgatt atgccctcct ggaactcaaa 850 aagccccaca agagaaaatt tatgaagatt ggggtgagcc ctcctgctaa 900 gcagctgcca gggggcagaa ttcacttctc tggttatgac aatgaccgac 950 caggcaattt ggtgtatcgc ttctgtgacg tcaaagacga gacctatgac 1000 ttgctctacc agcaatgcga tgcccagcca ggggccagcg ggtctggggt 1050 ctatgtgagg atgtggaaga gacagcagca gaagtgggag cgaaaaatta 1100 ttggcatttt ttcagggcac cagtgggtgg acatgaatgg ttccccacag 1150 gatttcaacg tggctgtcag aatcactcct ctcaaatatg cccagatttg 1200 ctattggatt aaaggaaact acctggattg tagggagggg tgacacagtg 1250 ttccctcctg gcagcaatta agggtcttca tgttcttatt ttaggagaggg 1300 ccaaattgtt ttttgtcatt ggcgtgcaca cgtgtgtgtg tgtgtgtgg 1350 tgtgtgtaag gtgtcttata atcttttacc tatttcttac aattgcaaga 1400 tgactggctt tactatttga aaactggttt gtgtatcata tcatataca 1450 tttaagcagt ttgaaggcat acttttgcat agaaataaaa aaaatactga 1500 tttggggcaa tgaggaatat ttgacaatta agttaatctt cacgtttttg 1550 caaactttga ttttattc atctgaactt gtttcaaaga tttatattaa 1600 atatttggca tacaagagat atgaaaaaaa aaaaaaaa 1638

<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

Met Ala Gly Ile Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu 1 5 10 15

Cys Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro 20 25 30

Thr Trp Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr 35 40 45

Leu Asn Leu Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu
50 55 60

Val Ser Ser Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu 65 70 75

Pro Thr Tyr Glu Glu Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu 80 85 90

Tyr Ala Asn Gly Ser Arg Thr Glu Thr Gln Val Gly Ile Tyr Ile

95 100 105

Leu Ser Ser Ser Gly Asp Gly Ala Gln His Arg Asp Ser Gly Ser 110 115 120

Ser	Gly	Lys	Ser	Arg 125	Arg	Lys	Arg	Gln	Ile 130	Tyr	Gly	Tyr	Asp	Ser 135
Arg	Phe	Ser	Ile	Phe 140	Gly	Lys	Asp	Phe	Leu 145	Leu	Asn	Tyr	Pro	Phe 150
Ser	Thr	Ser	Val	Lys 155	Leu	Ser	Thr	Gly	Cys 160	Thr	Gly	Thr	Leu	Val 165
Ala	Glu	Lys	His	Val 170	Leu	Thr	Ala	Ala	His 175	Cys	Ile	His	Asp	Gly 180
Lys	Thr	Tyr	Val	Lys 185	Gly	Thr	Gln	Lys	Leu 190	Arg	Val	Gly	Phe	Leu 195
Lys	Pro	Lys	Phe	Lys 200	Asp	Gly	Gly	Arg	Gly 205	Ala	Asn	Asp	Ser	Thr 210
Ser	Ala	Met	Pro	Glu 215	Gln	Met	Lys	Phe	Gln 220	Trp	Ile	Arg	Val	Lys 225
Arg	Thr	His	Val	Pro 230	Lys	Gly	Trp	Ile	Lys 235	Gly	Asn	Ala	Asn	Asp 240
Ile	Gly	Met	Asp	Tyr 245	Asp	Tyr	Ala	Leu	Leu 250	Glu	Leu	Lys	Lys	Pro 255
His	Lys	Arg	Lys	Phe 260	Met	Lys	Ile	Gly	Val 265	Ser	Pro	Pro	Ala	Lys 270
Gln	Leu	Pro	Gly	Gly 275	Arg	Ile	His	Phe	Ser 280	Gly	Tyr	Asp	Asn	Asp 285
Arg	Pro	Gly	Asn	Leu 290	Val	Tyr	Arg	Phe	Cys 295	Asp	Val	Lys	Asp	Gl·u 300
Thr	Tyr	Asp	Leu	Leu 305	Tyr	Gln	Gln	Cys	Asp 310	Ala	Gln	Pro	Gly	Ala 315
Ser	Gly	Ser	Gly	Val 320	Tyr	Val	Arg	Met	Trp 325	Lys	Arg	Gln	Gln	Gln 330
Lys	Trp	Glu	Arg	Lys 335	Ile	Ile	Gly	Ile	Phe 340	Ser	Gly	His	Gln	Trp 345
Val	Asp	Met	Asn	Gly 350	Ser	Pro	Gln	Asp	Phe 355	Asn	Val	Ala	Val	Arg 360
Ile	Thr	Pro	Leu	Lys 365	Tyr	Ala	Gln	Ile	Cys 370	Tyr	Trp	Ile	Lys	Gly 375
Asn	Tyr	Leu	Asp	Cys 380	Arg	Glu	Gly							

<210> 262

<211> 1378

<212> DNA

<213> Homo Sapien

<400> 262 gcatcgccct gggtctctcg agcctgctgc ctgctccccc gccccaccag 50 ccatggtggt ttctggagcg cccccagccc tgggtggggg ctgtctcggc 100 accttcacct ccctgctgct gctggcgtcg acagccatcc tcaatgcggc 150 caggatacet gttcccccag cetgtgggaa geeccageag etgaaceggg 200 ttgtgggcgg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250 atccagaaga atgggaccca ccactgcgca ggttctctgc tcaccagccg 300 ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaaccat 350 acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400 cggtcccaga aggtgggtgt tgcctgggtg gagccccacc ctgtgtattc 450 ctggaaggaa ggtgcctgtg cagacattgc cctggtgcgt ctcgagcgct 500 ccatacagtt ctcagagegg gtcctgccca tctgcctacc tgatgcctct 550 atccacctcc ctccaaacac ccactgctgg atctcaggct gggggagcat 600 ccaagatgga gttcccttgc cccaccctca gaccctgcag aagctgaagg 650 ttcctatcat cgactcggaa gtctgcagcc atctgtactg gcggggagca 700 ggacagggac ccatcactga ggacatgctg tgtgccggct acttggaggg 750 ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800 tggacggcgc ctggctgctg gccggcatca tcagctgggg cgagggctgt 850 geogagegea acaggeoegg ggtetacate ageotetetg egeacegete 900 ctgggtggag aagatcgtgc aaggggtgca gctccgcggg cgcgctcagg 950 ggggtggggc cctcagggca ccgagccagg gctctggggc cgccgcgcgc 1000 tectagggeg cagegggaeg egggetegg atetgaaagg eggeeagate 1050 cacatetgga tetggatetg eggeggeete gggeggttte eccegeegta 1100 aataggetea tetaceteta eetetggggg eeeggaegge tgetgeggaa 1150

aggaaacecc ctccccgacc cgcccgacgg cctcaggccc ccctccaagg 1200 catcaggeec egeceaacgg ceteatgtee eegeceecae gaetteegge 1250 cccgccccg ggccccagcg cttttgtgta tataaatgtt aatgattttt 1300 ataggtattt gtaaccctgc ccacatatct tatttattcc tccaatttca 1350 ataaattatt tattctccaa aaaaaaaa 1378

<210> 263

<211> 317

<212> PRT

<213> Homo Sapien

<400> 263 Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu 5 Gly Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu 20 Asn Ala Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile Val Ser Ile Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu Leu Thr Ser Arg Trp Val Ile Thr Ala Ala His 90 Cys Phe Lys Asp Asn Leu Asn Lys Pro Tyr Leu Phe Ser Val Leu Leu Gly Ala Trp Gln Leu Gly Asn Pro Gly Ser Arg Ser Gln Lys 115 Val Gly Val Ala Trp Val Glu Pro His Pro Val Tyr Ser Trp Lys 125 Glu Gly Ala Cys Ala Asp Ile Ala Leu Val Arg Leu Glu Arg Ser Ile Gln Phe Ser Glu Arg Val Leu Pro Ile Cys Leu Pro Asp Ala

Ser Ile His Leu Pro Pro Asn Thr His Cys Trp Ile Ser Gly Trp

160

175

165

180

155

170

```
Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro Gln Thr Leu
                 185
                                     190
                                                          195
Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His
                                     205
Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met
Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly
Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu
Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn
                                                          270
                 260
                                      265
Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val
                 275
Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly
Gly Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala
                                                          315
Arg Ser
<210> 264
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 264
gtccgcaagg atgcctacat gttc 24
<210> 265
<211> 19
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 265
gcagaggtgt ctaaggttg 19
<210> 266
<211> 24
```

```
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 266
agetetagae caatgeeage ttee 24
<210> 267
<211> 45
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
gccaccaact cctgcaagaa cttctcagaa ctgcccctgg tcatg 45
<210> 268
<211> 25
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<40,0> 268
ggggaattca ccctatgaca ttgcc 25
<210> 269
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 269
gaatgccctg caagcatcaa ctgg 24
<210> 270
<211> 50
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 270
 gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50
```

```
<210> 271
<211> 26
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 271
gcggaagggc agaatgggac tccaag 26
<210> 272
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 272
 cagccctgcc acatgtgc 18
<210> 273
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 273
 tactgggtgg tcagcaac 18
<210> 274
<211> 24
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 274
 ggcgaagagc agggtgagac cccg 24
<210> 275
<211> 45
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
```

```
<400> 275
gccctcatcc tctctggcaa atgcagttac agcccggagc ccgac 45
<210> 276
<211> 21
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 276
gggcagggat tccagggctc c 21
<210> 277
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 277
ggctatgaca gcaggttc 18
<210> 278
<211> 18
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 278
tgacaatgac cgaccagg 18
<210> 279
<211> 24
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 279
 gcatcgcatt gctggtagag caag 24
<210> 280
<211> 45
<212> DNA
<213> Artificial Sequence
<220>
```

```
<223> Synthetic Oligonucleotide Probe
ttacagtgcc ccctggaaac ccacttggcc tgcataccgc ctccc 45
<210> 281
<211> 34
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 281
cgtctcgagc gctccataca gttcccttgc ccca 34
<210> 282
<211> 61
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 282
 tggagggga gcgggatgct tgtctgggcg actccggggg ccccctcatg 50
tgccaggtgg a 61
<210> 283
<211> 119
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 283
 ccctcagacc ctgcagaagc tgaaggttcc tatcatcgac tcggaagtct 50
 gcagccatct gtactggcgg ggagcaggac agggacccat cactgaggac 100
 atgctgtgtg ccggctact 119
<210> 284
<211> 1875
<212> DNA
<213> Homo Sapien
<400> 284
 gacggctggc caccatgcac ggctcctgca gtttcctgat gcttctgctg 50
 ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100
```

agatgaggag aaacgtttga tggtggagct gcacaacctc taccgggccc 150 aggtatecee gaeggeetea gaeatgetge acatgagatg ggaegaggag 200 ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt ggggccacaa 250 caaggagege gggegeege gegagaatet gttegeeate acagaegagg 300 gcatggacgt gccgctggcc atggaggagt ggcaccacga gcgtgagcac 350 tacaacetea gegeegeeac etgeageeea ggeeagatgt geggeeacta 400 cacgcaggtg gtatgggcca agacagagag gatcggctgt ggttcccact 450 tctgtgagaa gctccagggt gttgaggaga ccaacatcga attactggtg 500 tgcaactatg agcctccggg gaacgtgaag gggaaacggc cctaccagga 550 ggggactecg tgctcccaat gtccctctgg ctaccactgc aagaactece 600 totgtgaacc catcggaagc coggaagatg ctcaggattt gccttacctg 650 gtaactgagg ccccatcctt ccgggcgact gaagcatcag actctaggaa 700 aatgggtact cettetteee tageaacggg gatteegget ttettggtaa 750 caqaqqtctc aqqctccctg gcaaccaagg ctctgcctgc tgtggaaacc 800 caggececaa etteettage aacgaaagae eegeeeteea tggeaacaga 850 ggctccacct tgcgtaacaa ctgaggtccc ttccattttg gcagctcaca 900 gcctgccctc cttggatgag gagccagtta ccttccccaa atcgacccat 950 gttcctatcc caaaatcagc agacaaagtg acagacaaaa caaaagtgcc 1000 ctctaggagc ccagagaact ctctggaccc caagatgtcc ctgacagggg 1050 caagggaact cctaccccat gcccaggagg aggctgaggc tgaggctgag 1100 ttgcctcctt ccagtgaggt cttggcctca gtttttccag cccaggacaa 1150 gccaggtgag ctgcaggcca cactggacca cacggggcac acctcctcca 1200 agtccctgcc caatttcccc aatacctctg ccaccgctaa tgccacgggt 1250 gggcgtgccc tggctctgca gtcgtccttg ccaggtgcag agggccctga 1300 caagectage gttgtgteag ggetgaacte gggeeetggt catgtgtggg 1350 geoeteteet gggaetactg etectgeete etetggtgtt ggetggaate 1400 ttctgaatgg gataccactc aaagggtgaa gaggtcagct gtcctcctgt 1450
catcttcccc accetgtccc cagcccctaa acaagatact tcttggttaa 1500
ggccctccgg aagggaaagg ctacggggca tgtgcctcat cacaccatcc 1550
atcctggagg cacaaggcct ggctggctgc gagctcagga ggccgcctga 1600
ggactgcaca ccgggcccac acctctcctg cccctccctc ctgagtcctg 1650
ggggtgggag gatttgaggg agctcactgc ctacctggcc tggggctgtc 1700
tgcccacaca gcatgtgcgc tctccctgag tgcctgtaa gctggggatg 1750
gggattccta ggggcagatg aaggacaagc cccactggag tggggttctt 1800
tgagtgggg aggcaggac gagggaagga aagtaactcc tgactccca 1850
ataaaaacct gtccaacctg tgaaa 1875

<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

Met His Gly Ser Cys Ser Phe Leu Met Leu Leu Leu Pro Leu Leu
1 5 10 15

Leu Leu Leu Val Ala Thr Thr Gly Pro Val Gly Ala Leu Thr Asp 20 25 30

Glu Glu Lys Arg Leu Met Val Glu Leu His Asn Leu Tyr Arg Ala \$35\$ 40 45

Gln Val Ser Pro Thr Ala Ser Asp Met Leu His Met Arg Trp Asp
50 55 60

Glu Glu Leu Ala Ala Phe Ala Lys Ala Tyr Ala Arg Gln Cys Val 65 70 75

Trp Gly His Asn Lys Glu Arg Gly Arg Arg Gly Glu Asn Leu Phe 80 85 90

Ala Ile Thr Asp Glu Gly Met Asp Val Pro Leu Ala Met Glu Glu 95 100 105

Trp His His Glu Arg Glu His Tyr Asn Leu Ser Ala Ala Thr Cys
110 115 120

Ser Pro Gly Gln Met Cys Gly His Tyr Thr Gln Val Val Trp Ala 125 130 135

Lys	Thr	Glu	Arg	Ile 140	Gly	Cys	Gly	Ser	His 145	Phe	Cys	Glu	Lys	Leu 150
Gln	Gly	Val	Glu	Glu 155	Thr	Asn	Ile	Glu	Leu 160	Leu	Val	Cys	Asn	Tyr 165
Glu	Pro	Pro	Gly	Asn 170	Val	Lys	Gly	Lys	Arg 175	Pro	Tyr	Gln	Glu	Gly 180
Thr	Pro	Cys	Ser	Gln 185	Cys	Pro	Ser	Gly	Tyr 190	His	Cys	Lys	Asn	Ser 195
Leu	Cys	Glu	Pro	Ile 200	Gly	Ser	Pro	Glu	Asp 205	Ala	Gln	Asp	Leu	Pro 210
Tyr	Leu	Val	Thr	Glu 215	Ala	Pro	Ser	Phe	Arg 220	Ala	Thr	Glu	Ala	Ser 225
Asp	Ser	Arg	Lys	Met 230	Gly	Thr	Pro	Ser	Ser 235	Leu	Ala	Thr	Gly	Ile 240
Pro	Ala	Phe	Leu	Val 245	Thr	Glu	Val	Ser	Gly 250	Ser	Leu	Ala	Thr	Lys 255
Ala	Leu	Pro	Ala	Val 260	Glu	Thr	Gln	Ala	Pro 265	Thr	Ser	Leu	Ala	Thr 270
Lys	Asp	Pro	Pro	Ser 275	Met	Ala	Thr	Glu	Ala 280	Pro	Pro	Cys	Val	Thr 285
Thr	Glu	Val	Pro	Ser 290	Ile	Leu	Ala	Ala	His 295	Ser	Leu	Pro	Ser	Leu 300
Asp	Glu	Glu	Pro	Val 305	Thr	Phe	Pro	Lys	Ser 310	Thr	His	Val	Pro	Ile 315
Pro	Lys	Ser	Ala	Asp 320	Lys	Val	Thr	Asp	Lys 325	Thr	Lys	Val	Pro	Ser 330
Arg	Ser	Pro	Glu	Asn 335	Ser	Leu	Asp	Pro	Lys 340	Met	Ser	Leu	Thr	Gly 345
Ala	Arg	Glu	Leu	Leu 350	Pro	His	Ala	Gln	Glu 355	Glu	Ala	Glu	Ala	Glu 360
Ala	Glu	Leu	Pro	Pro 365	Ser	Ser	Glu	Val	Leu 370	Ala	Ser	Val	Phe	Pro 375
Ala	Gln	Asp	Lys	Pro 380	Gly	Glu	Leu	Gln	Ala 385	Thr	Leu	Asp	His	Thr 390
Gly	His	Thr	Ser	Ser 395	Lys	Ser	Leu	Pro	Asn 400	Phe	Pro	Asn	Thr	Ser 405

```
Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser
                                     415
 Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser
                                     430
                 425
Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly
                 440
                                     445
Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe
                 455
<210> 286
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 286
tcctgcagtt tcctgatgc 19
<210> 287
<211> 24
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 287
 ctcatattgc acaccagtaa ttcg 24
<210> 288
<211> 45
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 288
 atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45
<210> 289
<211> 3662
<212> DNA
<213> Homo Sapien
<400> 289
 gtaactgaag tcaggctttt catttgggaa gccccctcaa cagaattcgg 50
```

tcattctcca agttatggtg gacgtacttc tgttgttctc cctctgcttg 100 ctttttcaca ttagcagacc ggacttaagt cacaacagat tatctttcat 150 caaggcaagt tccatgagcc accttcaaag ccttcgagaa gtgaaactga 200 acaacaatga attggagacc attccaaatc tgggaccagt ctcggcaaat 250 attacacttc tctccttggc tggaaacagg attgttgaaa tactccctga 300 acatctgaaa gagtttcagt cccttgaaac tttggacctt agcagcaaca 350 atatttcaga gctccaaact gcatttccag ccctacagct caaatatctg 400 tatctcaaca gcaaccgagt cacatcaatg gaacctgggt attttgacaa 450 tttggccaac acactccttg tgttaaagct gaacaggaac cgaatctcag 500 ctatcccacc caagatgttt aaactgcccc aactgcaaca tctcgaattg 550 aaccgaaaca agattaaaaa tgtagatgga ctgacattcc aaggccttgg 600 tgctctgaag tctctgaaaa tgcaaagaaa tggagtaacg aaacttatgg 650 atggagettt ttgggggetg ageaacatgg aaattttgca getggaecat 700 aacaacctaa cagagattac caaaggctgg ctttacggct tgctgatgct 750 gcaggaactt catctcagcc aaaatgccat caacaggatc agccctgatg 800 cctqqqaqtt ctqccaqaaq ctcaqtqaqc tqqacctaac tttcaatcac 850 ttatcaaggt tagatgattc aagctteett ggeetaaget tactaaatac 900 actgcacatt gggaacaaca gagtcagcta cattgctgat tgtgccttcc 950 gggggctttc cagtttaaag actttggatc tgaagaacaa tgaaatttcc 1000 tggactattg aagacatgaa tggtgctttc tctgggcttg acaaactgag 1050 gcgactgata ctccaaggaa atcggatccg ttctattact aaaaaagcct 1100 tcactggttt ggatgcattg gagcatctag acctgagtga caacgcaatc 1150 atgtctttac aaggcaatgc attttcacaa atgaagaaac tgcaacaatt 1200 gcatttaaat acatcaagcc ttttgtgcga ttgccagcta aaatggctcc 1250 cacagtgggt ggcggaaaac aactttcaga gctttgtaaa tgccagttgt 1300 gcccatcctc agctgctaaa aggaagaagc atttttgctg ttagcccaga 1350

tggctttgtg tgtgatgatt ttcccaaacc ccagatcacg gttcagccag 1400 aaacacagtc ggcaataaaa ggttccaatt tgagtttcat ctgctcagct 1450 gccaqcagca gtgattcccc aatgactttt gcttggaaaa aagacaatga 1500 actactgcat gatgctgaaa tggaaaatta tgcacacctc cgggcccaag 1550 gtggcgaggt gatggagtat accaccatcc ttcggctgcg cgaggtggaa 1600 tttgccagtg aggggaaata tcagtgtgtc atctccaatc actttggttc 1650 atcctactct gtcaaagcca agcttacagt aaatatgctt ccctcattca 1700 ccaagacccc catggatete accateegag etggggeeat ggeaegettg 1750 gagtgtgctg ctgtggggca cccagccccc cagatagcct ggcagaagga 1800 tgggggcaca gacttcccag ctgcacggga gagacgcatg catgtgatgc 1850 ccgaggatga cgtgttcttt atcgtggatg tgaagataga ggacattggg 1900 gtatacaget geacagetea gaacagtgea ggaagtattt cageaaatge 1950 aactctgact gtcctagaaa caccatcatt tttgcggcca ctgttggacc 2000 gaactgtaac caagggagaa acagccgtcc tacagtgcat tgctggagga 2050 agccctcccc ctaaactgaa ctggaccaaa gatgatagcc cattggtggt 2100 aaccgagagg cacttttttg cagcaggcaa tcagcttctg attattgtgg 2150 actcagatgt cagtgatgct gggaaataca catgtgagat gtctaacacc 2200 cttggcactg agagaggaaa cgtgcgcctc agtgtgatcc ccactccaac 2250 ctgcgactcc cctcagatga cagccccatc gttagacgat gacggatggg 2300 ccactgtggg tgtcgtgatc atagccgtgg tttgctgtgt ggtgggcacg 2350 tcactcgtgt gggtggtcat catataccac acaaggcgga ggaatgaaga 2400 ttgcagcatt accaacacag atgagaccaa cttgccagca gatattccta 2450 gttatttgtc atctcaggga acgttagctg acaggcagga tgggtacgtg 2500 tetteagaaa gtggaageea eeaceagttt gteacatett eaggtgetgg 2550 atttttctta ccacaacatg acagtagtgg gacctgccat attgacaata 2600 gcagtgaagc tgatgtggaa gctgccacag atctgttcct ttgtccgttt 2650 ttgggatcca caggccctat gtatttgaag ggaaatgtgt atggctcaga 2700

tccttttgaa acatatcata caggttgcag tcctgaccca agaacagttt 2750 taatqqacca ctatqaqccc aqttacataa agaaaaagga gtgctaccca 2800 tgttctcatc cttcagaaga atcctgcgaa cggagcttca gtaatatatc 2850 gtggccttca catgtgagga agctacttaa cactagttac tctcacaatg 2900 aaggacctgg aatgaaaaat ctgtgtctaa acaagtcctc tttagatttt 2950 aqtqcaaatc caqaqccagc qtcgqttgcc tcgagtaatt ctttcatggg 3000 tacctttgga aaagctctca ggagacctca cctagatgcc tattcaagct 3050 ttqqacaqcc atcagattgt cagccaagag ccttttattt gaaagctcat 3100 tetteeceaq aettggaete tgggteagag gaagatggga aagaaaggae 3150 agattttcag gaagaaaatc acatttgtac ctttaaacag actttagaaa 3200 actacaggac tccaaatttt cagtcttatg acttggacac atagactgaa 3250 tgagaccaaa ggaaaagctt aacatactac ctcaagtgaa cttttattta 3300 aaagagagag aatcttatgt tttttaaatg gagttatgaa ttttaaaaagg 3350 ataaaaatgc tttatttata cagatgaacc aaaattacaa aaagttatga 3400 aaatttttat actgggaatg atgctcatat aagaatacct ttttaaacta 3450 ttttttaact ttqttttatg caaaaaagta tcttacgtaa attaatgata 3500 taaatcatga ttattttatg tatttttata atgccagatt tctttttatg 3550 qaaaatqaqt tactaaagca ttttaaataa tacctgcctt gtaccatttt 3600 ttaaatagaa gttacttcat tatattttgc acattatatt taataaaatg 3650 tgtcaatttg aa 3662

Ile Ser Arg Pro Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys
20 25 30

<210> 290

<211> 1059

<212> PRT

<213> Homo Sapien

<400> 290

Met Val Asp Val Leu Leu Leu Phe Ser Leu Cys Leu Leu Phe His
1 5 10 15

Ala	Ser	Ser	Met	Ser 35	His	Leu	Gln	Ser	Leu 40	Arg	Glu	Val	Lys	Leu 45
Asn	Asn	Asn	Glu	Leu 50	Glu	Thr	Ile	Pro	Asn 55	Leu	Gly	Pro	Val	Ser 60
Ala	Asn	Ile	Thr	Leu 65	Leu	Ser	Leu	Ala	Gly 70	Asn	Arg	Ile	Val	Glu 75
Ile	Leu	Pro	Glu	His 80	Leu	Lys	Glu	Phe	Gln 85	Ser	Leu	Glu	Thr	Leu 90
Asp	Leu	Ser	Ser	Asn 95	Asn	Ile	*Ser	Glu	Leu 100	Gln	Thr	Ala	Phe	Pro 105
Ala	Leu	Gln	Leu	Lys 110	Tyr	Leu	Tyr	Leu	Asn 115	Ser	Asn	Arg	Val	Thr 120
Ser	Met	Glu	Pro	Gly 125	Tyr	Phe	Asp	Asn	Leu 130	Ala	Asn	Thr	Leu	Leu 135
Val	Leu	Lys	Leu	Asn 140	Arg	Asn	Arg	Ile	Ser 145	Ala	Ile	Pro	Pro	Lys 150
Met	Phe	Lys	Leu	Pro	Gln	Leu	Gln	His	Leu	Glu	Leu	Asn	Arg	Asn
				155					160					165
Lys	Ile	Lys	Asn	Val 170	Asp	Gly	Leu	Thr	Phe 175	Gln	Gly	Leu	Gly	Ala 180
Leu	Lys	Ser	Leu	Lys 185	Met	Gln	Arg	Asn	Gly 190	Val	Thr	Lys	Leu	Met 195
Asp	Gly	Ala	Phe	Trp 200	Gly	Leu	Ser	Asn	Met 205	Glu	Ile	Leu	Gln	Leu 210
Asp	His	Asn	Asn	Leu 215	Thr	Glu	Ile	Thr	Lys 220	Gly	Trp	Leu	Tyr	Gly 225
Leu	Leu	Met	Leu	Gln 230	Glu	Leu	His	Leu	Ser 235	Gln	Asn	Ala	Ile	Asn 240
Arg	Ile	Ser	Pro	Asp 245	Ala	Trp	Glu	Phe	Cys 250	Gln	Lys	Leu	Ser	Glu 255
Leu	Asp	Leu	Thr	Phe 260	Asn	His	Leu	Ser	Arg 265	Leu	Asp	Asp	Ser	Ser 270
Phe	Leu	Gly	Leu	Ser 275	Leu	Leu	Asn	Thr	Leu 280	His	Ile	Gly	Asn	Asn 285
Arg	Val	Ser	Tyr	Ile	Ala	Asp	Cys	Ala	Phe	Arg	Gly	Leu	Ser	Ser

				290					295					300
Leu	Lys	Thr	Leu	Asp 305	Leu	Lys	Asn	Asn	Glu 310	Ile	Ser	Trp	Thr	Ile 315
Glu	Asp	Met	Asn	Gly 320	Ala	Phe	Ser	Gly	Leu 325	Asp	Lys	Leu	Arg	Arg 330
Leu	Ile	Leu	Gln	Gly 335	Asn	Arg	Ile	Arg	Ser 340	Ile	Thr	Lys	Lys	Ala 345
Phe	Thr	Gly	Leu	Asp 350	Ala	Leu	Glu	His	Leu 355	Asp	Leu	Ser	Asp	Asn 360
Ala	Ile	Met	Ser	Leu 365	Gln	Gly	Asn	Ala	Phe 370	Ser	Gln	Met	Lys	Lys 375
Leu	Gln	Gln	Leu	His 380	Leu	Asn	Thr	Ser	Ser 385	Leu	Leu	Cys	Asp	Cys 390
Gln	Leu	Lys	Trp	Leu 395	Pro	Gln	Trp	Val	Ala 400	Glu	Asn	Asn	Phe	Gln 405
Ser	Phe	Val	Asn	Ala 410	Ser	Cys	Ala	His	Pro 415	Gln	Leu	Leu	Lys	Gly 420
Arg	Ser	Ile	Phe	Ala 425	Val	Ser	Pro	Asp	Gly 430	Phe	Val	Cys	Asp	Asp 435
Phe	Pro	Lys	Pro	Gln 440	Ile	Thr	Val	Gln	Pro 445	Gl u	Thr	Gln	Ser	Ala 450
Ile	Lys	Gly	Ser	Asn 455	Leu	Ser	Phe	Ile	Cys 460	Ser	Ala	Ala	Ser	Ser 465
Ser	Asp	Ser	Pro	Met	Thr	Phe	Ala	Trp	Lys	Lys	Asp	Asn	Glu	Leu
				470					475					480
Leu	His	Asp	Ala	Glu 485	Met	Glu	Asn	Tyr	Ala 490	His	Leu	Arg	Ala	Gln 495
Gly	Gly	Glu	Val	Met 500	Glu	Tyr	Thr	Thr	Ile 505	Leu	Arg	Leu	Arg	Glu 510
Val	Glu	Phe	Ala	Ser 515	Glu	Gly	Lys	Tyr	Gln 520	Cys	Val	Ile	Ser	Asn 525
His	Phe	Gly	Ser	Ser 530	Tyr	Ser	Val	Lys	Ala 535	Lys	Leu	Thr	Val	Asn 540
Met	Leu	Pro	Ser	Phe 545	Thr	Lys	Thr	Pro	Met 550	Asp	Leu	Thr	Ile	Arg 555



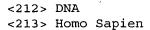


Ala Gly	Ala	Met	Ala 560	Arg	Leu	Glu	Cys	Ala 565	Ala	Val	Gly	His	Pro 570
Ala Pro	Gln	Ile	Ala 575	Trp	Gln	Lys	Asp	Gly 580	Gly	Thr	Asp	Phe	Pro 585
Ala Ala	Arg	Glu	Arg 590	Arg	Met	His	Val	Met 595	Pro	Glu	Asp	Asp	Val 600
Phe Phe	Ile	Val	Asp 605	Val	Lys	Ile	Glu	Asp 610	Ile	Gly	Val	Tyr	Ser 615
Cys Thr	Ala	Gln	Asn 620	Ser	Ala	Gly	Ser	Ile 625	Ser	Ala	Asn	Ala	Thr 630
Leu Thr	Val	Leu	Glu 635	Thr	Pro	Ser	Phe	Leu 640	Arg	Pro	Leu	Leu	Asp 645
Arg Thr	Val	Thr	Lys 650	Gly	Glu	Thr	Ala	Val 655	Leu	Gln	Cys	Ile	Ala 660
Gly Gly	Ser	Pro	Pro 665	Pro	Lys	Leu	Asn	Trp 670	Thr	Lys	Asp	Asp	Ser 675
Pro Leu	Val	Val	Thr 680	Glu	Arg	His	Phe	Phe 685	Ala	Ala	Gly	Asn	Gln 690
Leu Leu	Ile	Ile	Val 695	Asp	Ser	Asp	Val	Ser 700	Asp	Ala	Gly	Lys	Tyr 705
Thr Cys	Glu	Met	Ser 710	Asn	Thr	Leu	Gly	Thr 715		Arg	Gly	Asn	Val 720
Arg Leu	Ser	Val	Ile 725	Pro	Thr	Pro	Thr	Cys 730	Asp	Ser	Pro	Gln	Met 735
Thr Ala	Pro	Ser	Leu 740	Asp	Asp	Asp	Gly	Trp 745	Ala	Thr	Val	Gly	Val 750
Val Ile	Ile `	Ala	Val 755	Val	Cys	Cys	Val	Val 760	Gly	Thr	Ser	Leu	Val 765
Trp Val	Val	Ile	Ile 770	Tyr	His	Thr	Arg	Arg 775	Arg	Asn	Glu	Asp	Cys 780
Ser Ile	Thr	Asn	Thr 785	Asp	Glu	Thr	Asn	Leu 790	Pro	Ala	Asp	Ile	Pro 795
Ser Tyr	Leu	Ser		Gln	Gly	Thr	Leu		Asp	Arg	Gln	Asp	

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser 815 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr 830 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His 880 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr 895 890 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His 905 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn 935 940 945 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn 965 Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu 985 Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg 1000 Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly 1015 1010 Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn 1025 1030 His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro 1050 1045 Asn Phe Gln Ser Tyr Asp Leu Asp Thr

<210> 291 <211> 2906

1055



<400> 291 ggggagagga attgaccatg taaaaggaga ctttttttt tggtggtggt 50 ggctgttggg tgccttgcaa aaatgaagga tgcaggacgc agctttctcc 100 tggaaccgaa cgcaatggat aaactgattg tgcaagagag aaggaagaac 150 gaagettttt ettgtgagee etggatetta acacaaatgt gtatatgtge 200 acacagggag cattcaagaa tgaaataaac cagagttaga cccgcggggg 250 ttggtgtgtt ctgacataaa taaataatct taaagcagct gttcccctcc 300 ccacccccaa aaaaaaggat gattggaaat gaagaaccga ggattcacaa 350 agaaaaaagt atgttcattt ttctctataa aggagaaagt gagccaagga 400 gatatttttg gaatgaaaag tttggggctt ttttagtaaa gtaaagaact 450 aattaataat acatctgcaa agaaatttca gagaagaaaa gttgaccgcg 550 gcagattgag gcattgattg ggggagagaa accagcagag cacagttgga 600 tttgtgccta tgttgactaa aattgacgga taattgcagt tggatttttc 650 ttcatcaacc tcctttttt taaattttta ttccttttgg tatcaagatc 700 atgcgttttc tcttgttctt aaccacctgg atttccatct ggatgttgct 750 gtgatcagtc tgaaatacaa ctgtttgaat tccagaagga ccaacaccag 800 ataaattatg aatgttgaac aagatgacct tacatccaca gcagataatg 850 ataggteeta ggtttaacag ggeeetattt gaceeetge ttgtggtget 900 gctggctctt caacttcttg tggtggctgg tctggtgcgg gctcagacct 950 gcccttctgt gtgctcctgc agcaaccagt tcagcaaggt gatttgtgtt 1000 cggaaaaacc tgcgtgaggt tccggatggc atctccacca acacacggct 1050 gctgaacctc catgagaacc aaatccagat catcaaagtg aacagcttca 1100 agcacttgag gcacttggaa atcctacagt tgagtaggaa ccatatcaga 1150 accattgaaa ttggggcttt caatggtctg gcgaacctca acactctgga 1200 actetttgae aategtetta etaceateee gaatggaget tttgtataet 1250

tgtctaaact gaaggagctc tggttgcgaa acaaccccat tgaaagcatc 1300 cottettatg ettttaacag aatteettet ttgegeegae tagaettagg 1350 ggaattgaaa agactttcat acatctcaga aggtgccttt gaaggtctgt 1400 ccaacttgag gtatttgaac cttgccatgt gcaaccttcg ggaaatccct 1450 aacctcacac cgctcataaa actagatgag ctggatcttt ctgggaatca 1500 tttatctgcc atcaggcctg gctctttcca gggtttgatg caccttcaaa 1550 aactgtggat gatacagtcc cagattcaag tgattgaacg gaatgccttt 1600 gacaacette agteactagt ggagateaac etggeacaca ataatetaac 1650 attactgcct catgacctct tcactccctt gcatcatcta gagcggatac 1700 atttacatca caaccettgg aactgtaact gtgacatact gtggctcagc 1750 tggtggataa aagacatggc cccctcgaac acagcttgtt gtgcccggtg 1800 taacactcct cccaatctaa aggggaggta cattggagag ctcgaccaga 1850 attacttcac atgctatgct ccggtgattg tggagccccc tgcagacctc 1900 aatgtcactg aaggcatggc agctgagctg aaatgtcggg cctccacatc 1950 cctgacatct gtatcttgga ttactccaaa tggaacagtc atgacacatg 2000 qqqcqtacaa aqtqcggata gctgtgctca gtgatggtac gttaaatttc 2050 acaaatgtaa ctgtgcaaga tacaggcatg tacacatgta tggtgagtaa 2100 ttccgttggg aatactactg cttcagccac cctgaatgtt actgcagcaa 2150 ccactactcc tttctcttac ttttcaaccg tcacagtaga gactatggaa 2200 ccgtctcagg atgaggcacg gaccacagat aacaatgtgg gtcccactcc 2250 agtggtcgac tgggagacca ccaatgtgac cacctctctc acaccacaga 2300 gcacaaggtc gacagagaaa accttcacca tcccagtgac tgatataaac 2350 agtgggatcc caggaattga tgaggtcatg aagactacca aaatcatcat 2400 tgggtgtttt gtggccatca cactcatggc tgcagtgatg ctggtcattt 2450 tctacaagat gaggaagcag caccatcggc aaaaccatca cgccccaaca 2500 aggactgttg aaattattaa tgtggatgat gagattacgg gagacacacc 2550 catggaaagc cacctgccca tgcctgctat cgagcatgag cacctaaatc 2600 actataactc atacaaatct cccttcaacc acacaacaac agttaacaca 2650 ataaattcaa tacacagttc agtgcatgaa ccgttattga tccgaatgaa 2700 ctctaaagac aatgtacaag agactcaaat ctaaaacatt tacagagtta 2750 caaaaaacaa acaatcaaaa aaaaagacag tttattaaaa atgacacaaa 2800 tgactggct aaatctactg tttcaaaaaa gtgtctttac aaaaaaacaa 2850 aaaagaaaag aaatttattt attaaaaatt ctattgtgat ctaaagcaga 2900 caaaaa 2906

<210> 292

<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

Met Leu Asn Lys Met Thr Leu His Pro Gln Gln Ile Met Ile Gly
1 5 10 15

Pro Arg Phe Asn Arg Ala Leu Phe Asp Pro Leu Leu Val Val Leu 20 25 30

Leu Ala Leu Gln Leu Leu Val Val Ala Gly Leu Val Arg Ala Gln
35 40 45

Thr Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val
50 55 60

Ile Cys Val Arg Lys Asn Leu Arg Glu Val Pro Asp Gly Ile Ser
65 70 75

Thr Asn Thr Arg Leu Leu Asn Leu His Glu Asn Gln Ile Gln Ile 80 85 90

Ile Lys Val Asn Ser Phe Lys His Leu Arg His Leu Glu Ile Leu
95 100 105

Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe
110 115 120

Asn Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg 125 130 135

Leu Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu 140 145 150

Lys Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser

				155					160					165
Tyr	Ala	Phe	Asn	Arg 170	Ile	Pro	Ser	Leu	Arg 175	Arg	Leu	Asp	Leu	Gly 180
Glu	Leu	Lys	Arg	Leu 185	Ser	Tyr	Ile	Ser	Glu 190	Gly	Ala	Phe	Glu	Gly 195
Leu	Ser	Asn	Leu	Arg 200	Tyr	Leu	Asn	Leu	Ala 205	Met	Cys	Asn	Leu	Arg 210
Glu	Ile	Pro	Asn	Leu 215	Thr	Pro	Leu	Ile	Lys 220	Leu	Asp	Glu	Leu	Asp 225
Leu	Ser	Gly	Asn	His 230	Leu	Ser	Ala	Ile	Arg 235	Pro	Gly	Ser	Phe	Gln 240
Gly	Leu	Met	His	Leu 245	Gln	Lys	Leu	Trp	Met 250	Ile	Gln	Ser	Gln	Ile 255
Gln	Val	Ile	Glu	Arg 260	Asn	Ala	Phe	Asp	Asn 265	Leu	Gln	Ser	Leu	Val 270
Glu	Ile	Asn	Leu	Ala 275	His	Asn	Asn	Leu	Thr 280	Leu	Leu	Pro	His	Asp 285
Leu	Phe	Thr	Pro	Leu 290	His	His	Leu	Glu	Arg 295	Ile	His	Leu	His	His 300
Asn	Pro	Trp	Asn	Cys 305	Asn	Cys	Asp	Ile	Leu 310	Trp	Leu	Ser	Trp	Trp 315
Ile	Lys	Asp	Met	Ala 320	Pro	Ser	Asn	Thr	Ala 325	Cys	Cys	Ala	Arg	Cys 330
Asn	Thr	Pro	Pro	Asn 335	Leu	Lys	Gly	Arg	Tyr 340	Ile	Gly	Glu	Leu	Asp 345
Gln	Asn	Tyr	Phe	Thr 350		Tyr	Ala	Pro	Val 355	Ile	Val	Glu	Pro	Pro 360
Ala	Asp	Leu	Asn	Val 365	Thr	Glu	Gly	Met	Ala 370	Ala	Glu	Leu	Lys	Cys 375
Arg	Ala	Ser	Thr	Ser 380	Leu	Thr	Ser	Val	Ser 385	Trp	Ile	Thr	Pro	Asn 390
Gly	Thr	Val	Met	Thr 395	His	Gly	Ala	Tyr	Lys 400	Val	Arg	Ile	Ala	Val 405
Leu	Ser	Asp	Gly	Thr 410	Leu	Asn	Phe	Thr	Asn 415	Val	Thr	Val	Gln	Asp 420

Thr	Gly	Met	Tyr	Thr 425	Cys	Met	Val	Ser	Asn 430	Ser	Val	Gly	Asn	Thr 435
Thr	Ala	Ser	Ala	Thr 440	Leu	Asn	Val	Thr	Ala 445	Ala	Thr	Thr	Thr	Pro 450
Phe	Ser	Tyr	Phe	Ser 455	Thr	Val	Thr	Val	Glu 460	Thr	Met	Glu	Pro	Ser 465
Gln	Asp	Glu	Ala	Arg 470	Thr	Thr	Asp	Asn	Asn 475	Val	Gly	Pro	Thr	Pro 480
Val	Val	Asp	Trp	Glu 485	Thr	Thr	Asn	Val	Thr 490	Thr	Ser	Leu	Thr	Pro 495
Gln	Ser	Thr	Arg	Ser 500	Thr	Glu	Lys	Thr	Phe 505	Thr	Ile	Pro	Val	Thr 510
Asp	Ile	Asn	Ser	Gly 515	Ile	Pro	Gly	Ile	Asp 520	Glu	Val	Met	Lys	Thr 525
Thr	Lys	Ile	Ile	Ile 530	Gly	Cys	Phe	Val	Ala 535	Ile	Thr	Leu	Met	Ala 540
Ala	Val	Met	Leu	Val 545	Ile	Phe	Tyr	Lys	Met 550	Arg	Lys	Gln	His	His 555
Arg	Gln	Asn	His	His 560	Ala	Pro	Thr	Arg	Thr 565	Val	Glu	Ile	Ile	Asn 570
Val	Asp	Asp	Glu	Ile 575	Thr	Gly	Asp	Thr	Pro 580	Met	Glu	Ser	His	Leu 585
Pro	Met	Pro	Ala	Ile 590	Glu	His	Glu	His	Leu 595	Asn	His	Tyr	Asn	Ser 600
Tyr	Lys	Ser	Pro	Phe 605	Asn	His	Thr	Thr	Thr 610	Val	Asn	Thr	Ile	Asn 615
Ser	Ile	His	Ser	Ser 620	Val	His	Glu	Pro	Leu 625	Leu	Ile	Arg	Met	Asn 630
Ser	Lys	Asp	Asn	Val 635	Gln	Glu	Thr	Gln	Ile 640					
. 0 1 0 .	20	_												

<210> 293

<211> 4053

<212> DNA

<213> Homo Sapien

<400> 293

agccgacgct gctcaagctg caactctgtt gcagttggca gttcttttcg 50

gtttccctcc tgctgtttgg gggcatgaaa gggcttcgcc gccgggagta 100 aaagaaggaa ttgaccgggc agcgcgaggg aggagcgcgc acgcgaccgc 150 gagggcgggc gtgcaccctc ggctggaagt ttgtgccggg ccccgagcgc 200 gegeeggetg ggagettegg gtagagaeet aggeegetgg accgegatga 250 gegegeegag ceteegtgeg egegeegegg ggttgggget getgetgtge 300 geggtgetgg ggegegetgg eeggteegae ageggeggte geggggaaet 350 cgggcagccc tctggggtag ccgccgagcg cccatgcccc actacctgcc 400 gctgcctcgg ggacctgctg gactgcagtc gtaagcggct agcgcgtctt 450 cccgagccac tcccgtcctg ggtcgctcgg ctggacttaa gtcacaacag 500 attatettte ateaaggeaa gtteeatgag eeacetteaa ageettegag 550 aagtgaaact gaacaacaat gaattggaga ccattccaaa tctgggacca 600 gtctcggcaa atattacact tctctccttg gctggaaaca ggattgttga 650 aatactccct gaacatctga aagagtttca gtcccttgaa actttggacc 700 ttagcagcaa caatatttca gagctccaaa ctgcatttcc agccctacag 750 ctcaaatatc tgtatctcaa cagcaaccga gtcacatcaa tggaacctgg 800 gtattttgac aatttggcca acacactcct tgtgttaaag ctgaacagga 850 accgaatctc agctatccca cccaagatgt ttaaactgcc ccaactgcaa 900 catctcgaat tgaaccgaaa caagattaaa aatgtagatg gactgacatt 950 ccaaggcctt ggtgctctga agtctctgaa aatgcaaaga aatggagtaa 1000 cgaaacttat ggatggagct ttttgggggc tgagcaacat ggaaattttg 1050 cagctggacc ataacaacct aacagagatt accaaaggct ggctttacgg 1100 cttgctgatg ctgcaggaac ttcatctcag ccaaaatgcc atcaacagga 1150 tcagccctga tgcctgggag ttctgccaga agctcagtga gctggaccta 1200 actttcaatc acttatcaag gttagatgat tcaagcttcc ttggcctaag 1250 cttactaaat acactgcaca ttgggaacaa cagagtcagc tacattgctg 1300 attgtgcctt ccgggggctt tccagtttaa agactttgga tctgaagaac 1350

aatgaaattt cctggactat tgaagacatg aatggtgctt tctctgggct 1400 tgacaaactg aggcgactga tactccaagg aaatcggatc cgttctatta 1450 ctaaaaaagc cttcactggt ttggatgcat tggagcatct agacctgagt 1500 gacaacgcaa tcatgtcttt acaaggcaat gcattttcac aaatgaagaa 1550 actgcaacaa ttgcatttaa atacatcaag ccttttgtgc gattgccagc 1600 taaaatggct cccacagtgg gtggcggaaa acaactttca gagctttgta 1650 aatgccagtt gtgcccatcc tcagctgcta aaaggaagaa gcatttttgc 1700 tgttagccca gatggctttg tgtgtgatga ttttcccaaa ccccagatca 1750 cggttcagcc agaaacacag tcggcaataa aaggttccaa tttgagtttc 1800 atctgctcag ctgccagcag cagtgattcc ccaatgactt ttgcttggaa 1850 aaaagacaat gaactactgc atgatgctga aatggaaaat tatgcacacc 1900 teegggeeca aggtggegag gtgatggagt ataccaccat cetteggetg 1950 cgcgaggtgg aatttgccag tgaggggaaa tatcagtgtg tcatctccaa 2000 tcactttggt tcatcctact ctgtcaaagc caagcttaca gtaaatatgc 2050 ttccctcatt caccaagacc cccatggatc tcaccatccg agctggggcc 2100 atggcacgct tggagtgtgc tgctgtgggg cacccagccc cccagatagc 2150 ctggcagaag gatgggggca cagacttccc agctgcacgg gagagacgca 2200 tgcatgtgat gcccgaggat gacgtgttct ttatcgtgga tgtgaagata 2250 gaggacattg gggtatacag ctgcacagct cagaacagtg caggaagtat 2300 ttcagcaaat gcaactctga ctgtcctaga aacaccatca tttttgcggc 2350 cactgttgga ccgaactgta accaagggag aaacagccgt cctacagtgc 2400 attgctggag gaagccctcc ccctaaactg aactggacca aagatgatag 2450 cccattggtg gtaaccgaga ggcacttttt tgcagcaggc aatcagcttc 2500 tgattattgt ggactcagat gtcagtgatg ctgggaaata cacatgtgag 2550 atgtctaaca cccttggcac tgagagagga aacgtgcgcc tcagtgtgat 2600 ccccactcca acctgcgact cccctcagat gacagcccca tcgttagacg 2650 atgacggatg ggccactgtg ggtgtcgtga tcatagccgt ggtttgctgt 2700

gtggtgggca cgtcactcgt gtgggtggtc atcatatacc acacaaggcg 2750 gaggaatgaa gattgcagca ttaccaacac agatgagacc aacttgccag 2800 cagatattcc tagttatttg tcatctcagg gaacgttagc tgacaggcag 2850 gatgggtacg tgtcttcaga aagtggaagc caccaccagt ttgtcacatc 2900 ttcaggtgct ggatttttct taccacaaca tgacagtagt gggacctgcc 2950 atattgacaa tagcagtgaa gctgatgtgg aagctgccac agatctgttc 3000 ctttgtccgt ttttgggatc cacaggccct atgtatttga agggaaatgt 3050 gtatggctca gatccttttg aaacatatca tacaggttgc agtcctgacc 3100 caagaacagt tttaatggac cactatgagc ccagttacat aaagaaaaag 3150 gagtgctacc catgttctca tccttcagaa gaatcctgcg aacggagctt 3200 cagtaatata tcgtggcctt cacatgtgag gaagctactt aacactagtt 3250 actctcacaa tgaaggacct ggaatgaaaa atctgtgtct aaacaagtcc 3300 tetttagatt ttagtgcaaa teeagageea gegteggttg eetegagtaa 3350 ttctttcatg ggtacctttg gaaaagctct caggagacct cacctagatg 3400 cctattcaag ctttggacag ccatcagatt gtcagccaag agccttttat 3450 ttgaaagete attetteece agaettggae tetgggteag aggaagatgg 3500 gaaagaaagg acagattttc aggaagaaaa tcacatttgt acctttaaac 3550 agactttaga aaactacagg actccaaatt ttcagtctta tgacttggac 3600 acatagactg aatgagacca aaggaaaagc ttaacatact acctcaagtg 3650 aacttttatt taaaagagag agaatcttat gttttttaaa tggagttatg 3700 aattttaaaa ggataaaaat gctttattta tacagatgaa ccaaaattac 3750 aaaaagttat gaaaattttt atactgggaa tgatgctcat ataagaatac 3800 ctttttaaac tatttttaa ctttgtttta tgcaaaaaag tatcttacgt 3850 aaattaatga tataaatcat gattatttta tgtatttta taatgccaga 3900 tttcttttta tggaaaatga gttactaaag cattttaaat aatacctgcc 3950 ttgtaccatt ttttaaatag aagttacttc attatatttt gcacattata 4000

aaa 4053

<210> 294

<211> 1119

<212> PRT <213> Homo Sapien

<400> 294

Met Ser Ala Pro Ser Leu Arg Ala Arg Ala Ala Gly Leu Gly Leu

1 5 10 15

Leu Leu Cys Ala Val Leu Gly Arg Ala Gly Arg Ser Asp Ser Gly

Gly Arg Gly Glu Leu Gly Gln Pro Ser Gly Val Ala Ala Glu Arg
35 40 45

Pro Cys Pro Thr Thr Cys Arg Cys Leu Gly Asp Leu Leu Asp Cys
50 55 60

Ser Arg Lys Arg Leu Ala Arg Leu Pro Glu Pro Leu Pro Ser Trp
65 70 75

Val Ala Arg Leu Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys 80 85 90

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu 95 100 105

Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser 110 115 120

Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu 125 130 135

Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu 140 145 150

Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro 155 160 165

Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr 170 175 180

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu 185 190 195

Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys 200 205 210

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn

				215					220					225
Lys	Ile	Lys	Asn	Val 230	Asp	Gly	Leu	Thr	Phe 235	Gln	Gly	Leu	Gly	Ala 240
Leu	Lys	Ser	Leu	Lys 245	Met	Gln	Arg	Asn	Gly 250	Val	Thr	Lys	Leu	Met 255
Asp	Gly	Ala	Phe	Trp 260	Gly	Leu	Ser	Asn	Met 265	Glu	Ile	Leu	Gln	Leu 270
Asp	His	Asn	Asn	Leu 275	Thr	Glu	Ile	Thr	Lys 280	Gly	Trp	Leu	Tyr	Gly 285
Leu	Leu	Met	Leu	Gln 290	Glu	Leu	His	Leu	Ser 295	Gln	Asn	Ala	Ile	Asn 300
Arg	Ile	Ser	Pro	Asp 305	Ala	Trp	Glu	Phe	Cys 310	Gln	Lys	Leu	Ser	Glu 315
Leu	Asp	Leu	Thr	Phe 320	Asn	His	Leu	Ser	Arg 325	Leu	Asp	Asp	Ser	Ser 330
Phe	Leu	Gly	Leu	Ser 335	Leu	Leu	Asn	Thr	Leu 340	His	Ile	Gly	Asn	Asn 345
Arg	Val	Ser	Tyr	Ile 350	Ala	Asp	Cys	Ala	Phe 355	Arg	Gly	Leu	Ser	Ser 360
Leu	Lys	Thr	Leu	Asp 365	Leu	Lys	Asn	Asn	Glu 370	Ile	Ser	Trp	Thr	Ile 375
Glu	Asp	Met	Asn	Gly 380	Ala	Phe	Ser	Gly	Leu 385	Asp	Lys	Leu	Arg	Arg 390
Leu	Ile	Leu	Gln	Gly 395	Asn	Arg	Ile	Arg	Ser 400	Ile	Thr	Lys	Lys	Ala 405
Phe	Thr	Gly	Leu	Asp 410	Ala	Leu	Glu	His	Leu 415	Asp	Leu	Ser	Asp	Asn 420
Ala	Ile	Met	Ser	Leu 425	Gln	Gly	Asn	Ala	Phe 430	Ser	Gln	Met	Lys	Lys 435
Leu	Gln	Gln	Leu	His 440	Leu	Asn	Thr	Ser	Ser 445	Leu	Leu	Cys	Asp	Cys 450
Gln	Leu	Lys	Trp	Leu 455	Pro	Gln	Trp	Val	Ala 460	Glu	Asn	Asn	Phe	Gln 465
Ser	Phe	Val	Asn	Ala 470	Ser	Cys	Ala	His	Pro 475	Gln	Leu	Leu	Lys	Gly 480

Arg	Ser	Ile	Phe	Ala 485	Val	Ser	Pro	Asp	Gly 490	Phe	Val	Cys	Asp	Asp 495
Phe	Pro	Lys	Pro	Gln 500	Ile	Thr	Val	Gln	Pro 505	Glu	Thr	Gln	Ser	Ala 510
Ile	Lys	Gly	Ser	Asn 515	Leu	Ser	Phe	Ile	Cys 520	Ser	Ala	Ala	Ser	Ser 525
Ser	Asp	Ser	Pro	Met 530	Thr	Phe	Ala	Trp	Lys 535	Lys	Asp	Asn	Glu	Leu 540
Leu	His	Asp	Ala	Glu 545	Met	Glu	Asn	Tyr	Ala 550	His	Leu	Arg	Ala	Gln 555
Gly	Gly	Glu	Val	Met 560	Glu	Tyr	Thr	Thr	Ile 565	Leu	Arg	Leu	Arg	Glu 570
Val	Glu	Phe	Ala	Ser 575	Glu	Gly	Lys	Tyr	Gln 580	Cys	Val	Ile	Ser	Asn 585
His	Phe	Gly	Ser	Ser 590	Tyr	Ser	Val	Lys	Ala 595	Lys	Leu	Thr	Val	Asn 600
Met	Leu	Pro	Ser	Phe 605	Thr	Lys	Thr	Pro	Met 610	Asp	Leu	Thr	Ile	Arg 615
Ala	Gly	Ala	Met	Ala 620	Arg	Leu	Glu	Cys	Ala 625	Ala	Val	Gly	His	Pro 630
Ala	Pro	Gln	Ile	Ala 635	Trp	Gln	Lys	Asp	Gly 640	Gly	Thr	Asp	Phe	Pro 645
Ala	Ala	Arg	Glu	Arg 650	Arg	Met	His	Val	Met 655	Pro	Glu	Asp	Asp	Val 660
Phe	Phe	Ile	Val	Asp 665	Val	Lys	Ile	Glu	Àsp 670	Ile	Gly	Val	Tyr	Ser 675
Cys	Thr	Ala	Gln	Asn 680	Ser	Ala	Gly	Ser	Ile 685	Ser	Ala	Asn	Ala	Thr 690
Leu	Thr	Val	Leu	Glu 695	Thr	Pro	Ser	Phe	Leu 700	Arg	Pro	Leu	Leu	Asp 705
Arg	Thr	Val	Thr	Lys 710	Gly	Glu	Thr	Ala	Val 715	Leu	Gln	Cys	Ile	Ala 720
Gly	Gly	Ser	Pro	Pro 725	Pro	Lys	Leu	Asn	Trp 730	Thr	Lys	Asp	Asp	Ser 735
Pro	Leu	Val	Val	Thr 740	Glu	Arg	His	Phe	Phe 745	Ala	Ala	Gly	Asn	Gln 750

Leu	Leu	Ile	Ile	Val 755	Asp	Ser	Asp	Val	Ser 760	Asp	Ala	Gly	Lys	Tyr 765
Thr	Cys	Glu	Met	Ser 770	Asn	Thr	Leu	Gly	Thr 775	Glu	Arg	Gly	Asn	Val 780
Arg	Leu	Ser	Val	Ile 785	Pro	Thr	Pro	Thr	Cys 790	Asp	Ser	Pro	Gln	Met 795
Thr	Ala	Pro	Ser	Leu 800	Asp	Asp	Asp	Gly	Trp 805	Ala	Thr	Val	Gly	Val 810
Val	Ile	Ile	Ala	Val 815	Val	Cys	Cys	Val	Val 820	Gly	Thr	Ser	Leu	Val 825
Trp	Val	Val	Ile	Ile 830	Tyr	His	Thr	Arg	Arg 835	Arg	Asn	Glu	Asp	Cys 840
Ser	Ile	Thr	Asn	Thr 845	Asp	Glu	Thr	Asn	Leu 850	Pro	Ala	Asp	Ile	Pro 855
Ser	Tyr	Leu	Ser	Ser 860	Gln	Gly	Thr	Leu	Ala 865	Asp	Arg	Gln	Asp	Gly 870
Tyr	Val	Ser	Ser	Glu 875	Ser	Gly	Ser	His	His 880	Gln	Phe	Val	Thr	Ser 885
Ser	Gly	Ala	Gly	Phe 890	Phe	Leu	Pro	Gln	His 895	Asp	Ser	Ser	Gly	Thr 900
Cys	His	Ile	Asp	Asn 905	Ser	Ser	Glu	Ala	Asp 910	Val	Glu	Ala	Ala	Thr 915
Asp	Leu	Phe	Leu	Cys 920	Pro	Phe	Leu	Gly	Ser 925	Thr	Gly	Pro	Met	Tyr 930
Leu	Lys	Gly	Asn	Val 935	Tyr	Gly	Ser	Asp	Pro 940	Phe	Glu	Thr	Tyr	His 945
Thr	Gly	Cys	Ser	Pro 950	Asp	Pro	Arg	Thr	Val 955	Leu	Met	Asp	His	Tyr 960
Glu	Pro	Ser	Tyr	Ile 965	Lys	Lys	Lys	Glu	Cys 970	Tyr	Pro	Cys	Ser	His 975
Pro	Ser	Glu	Glu	Ser 980	Cys	Glu	Arg	Ser	Phe 985	Ser	Asn	Ile	Ser	Trp 990
Pro	Ser	His	Val	Arg 995	Lys	Leu	Leu	Asn	Thr 1000	Ser	Tyr	Ser		Asn 1005
Glu	Gly	Pro	Gly	Met	Lys	Asn	Leu	Cys	Leu	Asn	Lys	Ser	Ser	Leu

1010 1015 102	0
Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser As 1025 1030 103	
Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Le 1040 1045 105	
Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Ar 1055 1060 106	
Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gl 1070 1075 108	
Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu As 1085 1090 109	
His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pr 1100 1105 111	
Asn Phe Gln Ser Tyr Asp Leu Asp Thr 1115	
<210> 295	
<211> 18	
<211> 10	
<213> Artificial Sequence	
<220>	
<223> Synthetic Oligonucleotide Probe	
<400> 295	
ggaaccgaat ctcagcta 18	
<210> 296	
<211> 19 <212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic Oligonucleotide Probe	
<400> 296	
cctaaactga actggacca 19	
<210> 297	
<211> 19	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic Oligonucleotide Probe	

```
<400> 297
 ggctggagac actgaacct 19
<210> 298
<211> 24
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 298
 acagetgeac ageteagaac agtg 24
<210> 299
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 299
 cattcccagt ataaaaattt tc 22
. <210> 300
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 300
 gggtcttggt gaatgagg 18
<210> 301
<211> 24
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 301
 gtgcctctcg gttaccacca atgg 24
<210> 302
<211> 50
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Synthetic Oligonucleotide Probe
<400> 302
geggecactg ttggaccgaa ctgtaaccaa gggagaaaca geegteetac 50
<210> 303
<211> 28
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 303
gcctttgaca accttcagtc actagtgg 28
<210> 304
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 304
ccccatgtgt ccatgactgt tccc 24
<210> 305
<211> 45
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 305
 tactgcctca tgacctcttc actcccttgc atcatcttag agcgg 45
<210> 306
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 306
 actccaagga aatcggatcc gttc 24
<210> 307
<211> 24
```

```
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
<400> 307
ttagcagctg aggatgggca caac 24
<210> 308
<211> 24
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 308
actccaagga aatcggatcc gttc 24
<210> 309
<211> 50
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 309
gccttcactg gtttggatgc attggagcat ctagacctga gtgacaacgc 50
<210> 310
<211> 3296
<212> DNA
<213> Homo Sapien
<400> 310
 caaaacttgc gtcgcggaga gcgcccagct tgacttgaat ggaaggagcc 50
 cgagcccgcg gagcgcagct gagactgggg gagcgcgttc ggcctgtggg 100
 gegeegeteg gegeeggge geageaggga aggggaaget gtggtetgee 150
 ctgctccacg aggcgccact ggtgtgaacc gggagagccc ctgggtggtc 200
 ccqtccccta tccctccttt atatagaaac cttccacact gggaaggcag 250
 cggcgaggca ggagggctca tggtgagcaa ggaggccggc tgatctgcag 300
 gcgcacagca ttccgagttt acagattttt acagatacca aatggaaggc 350
 gaggaggcag aacagcctgc ctggttccat cagccctggc gcccaggcgc 400
```

atotgactog gcaccocotg caggoaccat ggcccagago cgggtgctgc 450 tgctcctgct gctgctgccg ccacagctgc acctgggacc tgtgcttgcc 500 gtgagggccc caggatttgg ccgaagtggc ggccacagcc tgagccccga 550 agagaacgaa tttgcggagg aggagccggt gctggtactg agccctgagg 600 agecegggee tggeceagee geggteaget geceeegaga etgtgeetgt 650 tcccaggagg gcgtcgtgga ctgtggcggt attgacctgc gtgagttccc 700 gggggacctg cctgagcaca ccaaccacct atctctgcag aacaaccagc 750 tggaaaagat ctaccctgag gagctctccc ggctgcaccg gctggagaca 800 ctgaacctgc aaaacaaccg cctgacttcc cgagggctcc cagagaaggc 850 gtttgagcat ctgaccaacc tcaattacct gtacttggcc aataacaagc 900 tgaccttggc accccgcttc ctgccaaacg ccctgatcag tgtggacttt 950 gctgccaact atctcaccaa gatctatggg ctcacctttg gccagaagcc 1000 aaacttgagg tetgtgtace tgeacaacaa caagetggea gaegeeggge 1050 tgccggacaa catgttcaac ggctccagca acgtcgaggt cctcatcctg 1100 tccagcaact tcctgcgcca cgtgcccaag cacctgccgc ctgccctgta 1150 caagetgeac etcaagaaca acaagetgga gaagateece eegggggeet 1200 tcagcgagct gagcagcctg cgcgagctat acctgcagaa caactacctg 1250 actgacgagg gcctggacaa cgagacette tggaagetet ccageetgga 1300 gtacctggat ctgtccagca acaacctgtc tcgggtccca gctgggctgc 1350 cgcgcagcct ggtgctgctg cacttggaga agaacgccat ccggagcgtg 1400 gacgcgaatg tgctgacccc catccgcagc ctggagtacc tgctgctgca 1450 cagcaaccag ctgcgggagc agggcatcca cccactggcc ttccagggcc 1500 tcaagcggtt gcacacggtg cacctgtaca acaacgcgct ggagcgcgtg 1550 cccagtggcc tgcctcgccg cgtgcgcacc ctcatgatcc tgcacaacca 1600 gatcacaggc attggccgcg aagactttgc caccacctac ttcctggagg 1650 ageteaacet cagetacaac egeateacea geceacaggt geacegegae 1700 gccttccgca agctgcgcct gctgcgctcg ctggacctgt cgggcaaccg 1750 gctgcacacg ctgccacctg ggctgcctcg aaatgtccat gtgctgaagg 1800 tcaagcgcaa tgagctggct gccttggcac gaggggcgct ggcgggcatg 1850 geteagetge gtgagetgta ceteaceage aacegaetge geageegage 1900 cctgggcccc cgtgcctggg tggacctcgc ccatctgcag ctgctggaca 1950 tegeegggaa teageteaca gagateeeeg aggggeteee egagteactt 2000 gagtacctgt acctgcagaa caacaagatt agtgcggtgc ccgccaatgc 2050 cttcgactcc acgcccaacc tcaaggggat ctttctcagg tttaacaagc 2100 tggctgtggg ctccgtggtg gacagtgcct tccggaggct gaagcacctg 2150 caggtcttgg acattgaagg caacttagag tttggtgaca tttccaagga 2200 aggaagagga aacaagatag tgacaaggtg atgcagatgt gacctaggat 2300 gatggaccgc cggactcttt tctgcagcac acgcctgtgt gctgtgagcc 2350 ccccactctg ccgtgctcac acagacacac ccagctgcac acatgaggca 2400 tcccacatga cacgggctga cacagtctca tatccccacc ccttcccacg 2450 gegtgtecca eggecagaca catgcacaca catcacacec teaaacacec 2500 ageteageea cacacaacta cectecaaac caccacagte tetgteacac 2550 ccccactacc gctgccacgc cctctgaatc atgcagggaa gggtctgccc 2600 ctgccctggc acacacaggc acccattccc tccccctgct gacatgtgta 2650 tgcgtatgca tacacaccac acacacaca atgcacaagt catgtgcgaa 2700 cageceteca aageetatge cacagacage tettgeecca gecagaatea 2750 gccatagcag ctcgccgtct gccctgtcca tctgtccgtc cgttccctgg 2800 agaagacaca agggtatcca tgctctgtgg ccaggtgcct gccaccctct 2850 ggaactcaca aaagctggct tttattcctt tcccatccta tggggacagg 2900 agecttcagg actgctggcc tggcctggcc caccctgctc ctccaggtgc 2950 tgggcagtca ctctgctaag agtccctccc tgccacgccc tggcaggaca 3000 caggeaettt tecaatggge aageeeagtg gaggeaggat gggagageee 3050

```
cctgggtgct gctggggcct tggggcagga gtgaagcaga ggtgatgggg 3100
 ctgggctgag ccagggagga aggacccagc tgcacctagg agacaccttt 3150
 gttcttcagg cctgtggggg aagttccggg tgcctttatt ttttattctt 3200
 ttctaaggaa aaaaatgata aaaatctcaa agctgatttt tcttgttata 3250
gaaaaactaa tataaaagca ttatccctat ccctgcaaaa aaaaaa 3296
<210> 311
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 311
gcattggccg cgagactttg cc 22
<210> 312
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 312
gcggccacgg tccttggaaa tg 22
<210> 313
<211> 45
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 313
tggaggagct caacctcagc tacaaccgca tcaccagccc acagg 45
<210> 314
<211> 3003
<212> DNA
<213> Homo Sapien
<400> 314
gggaggggc teegggegee gegeageaga cetgeteegg eegegegeet 50
```

cgccgctgtc ctccgggagc ggcagcagta gcccgggcgg cgagggctgg 100

gggttcctcg agactctcag aggggcgcct cccatcggcg cccaccaccc 150 caacctgttc ctcgcgcgcc actgcgctgc gccccaggac ccgctgccca 200 acatggattt teteetggeg etggtgetgg tateeteget etaeetgeag 250 geggeegeeg agttegaegg gaggtggeee aggeaaatag tgteategat 300 tggcctatgt cgttatggtg ggaggattga ctgctgctgg ggctgggctc 350 gccagtcttg gggacagtgt cagcctgtgt gccaaccacg atgcaaacat 400 ggtgaatgta tcgggccaaa caagtgcaag tgtcatcctg gttatgctgg 450 aaaaacctgt aatcaagatc taaatgagtg tggcctgaag ccccggccct 500 gtaagcacag gtgcatgaac acttacggca gctacaagtg ctactgtctc 550 aacggatata tgctcatgcc ggatggttcc tgctcaagtg ccctgacctg 600 ctccatggca aactgtcagt atggctgtga tgttgttaaa ggacaaatac 650 ggtgccagtg cccatcccct ggcctgcacc tggctcctga tgggaggacc 700 tgtgtagatg ttgatgaatg tgctacagga agagcctcct gccctagatt 750 taggcaatgt gtcaacactt ttgggagcta catctgcaag tgtcataaag 800 gcttcgatct catgtatatt ggaggcaaat atcaatgtca tgacatagac 850 qaatqctcac ttggtcagta tcagtgcagc agctttgctc gatgttataa 900 cgtacgtggg tcctacaagt gcaaatgtaa agaaggatac cagggtgatg 950 gactgacttg tgtgtatatc ccaaaagtta tgattgaacc ttcaggtcca 1000 attcatgtac caaagggaaa tggtaccatt ttaaagggtg acacaggaaa 1050 taataattgg attcctgatg ttggaagtac ttggtggcct ccgaagacac 1100 catatattcc tcctatcatt accaacaggc ctacttctaa gccaacaaca 1150 agacctacac caaagccaac accaattcct actccaccac caccaccacc 1200 cctgccaaca gagctcagaa cacctctacc acctacaacc ccagaaaggc 1250 caaccaccgg actgacaact atagcaccag ctgccagtac acctccagga 1300 gggattacag ttgacaacag ggtacagaca gaccctcaga aacccagagg 1350 agatgtgttc agtgttctgg tacacagttg taattttgac catggacttt 1400

gtggatggat cagggagaaa gacaatgact tgcactggga accaatcagg 1450 gacccagcag gtggacaata tctgacagtg tcggcagcca aagccccagg 1500 gggaaaagct gcacgcttgg tgctacctct cggccgcctc atgcattcag 1550 gggacctgtg cctgtcattc aggcacaagg tgacggggct gcactctggc 1600 acactccagg tgtttgtgag aaaacacggt gcccacggag cagccctgtg 1650 gggaagaaat ggtggccatg gctggaggca aacacagatc accttgcgag 1700 gggetgacat caagagegaa teacaaagat gattaaaggg ttggaaaaaa 1750 agatctatga tggaaaatta aaggaactgg gattattgag cctggagaag 1800 agaagactga ggggcaaacc attgatggtt ttcaagtata tgaagggttg 1850 gcacagagag ggtggcgacc agctgttctc catatgcact aagaatagaa 1900 caagaggaaa ctggcttaga ctagagtata agggagcatt tcttggcagg 1950 ggccattgtt agaatacttc ataaaaaaag aagtgtgaaa atctcagtat 2000 ctctctctt ttctaaaaaa ttagataaaa atttgtctat ttaagatggt 2050 taaagatgtt cttacccaag gaaaagtaac aaattataga atttcccaaa 2100 agatgttttg atcctactag tagtatgcag tgaaaatctt tagaactaaa 2150 taatttggac aaggettaat ttaggeattt eeetettgae eteetaatgg 2200 agagggattg aaaggggaag agcccaccaa atgctgagct cactgaaata 2250 tctctccctt atggcaatcc tagcagtatt aaagaaaaaa ggaaactatt 2300 tattccaaat gagagtatga tggacagata ttttagtatc tcagtaatgt 2350 cctagtgtgg cggtggtttt caatgtttct tcatggtaaa ggtataagcc 2400 ccttcaagga acacagttca gagagatttt catcgggtgc attctctctg 2500 cttcgtgtgt gacaagttat cttggctgct gagaaagagt gccctgcccc 2550 acaccggcag acctttcctt cacctcatca gtatgattca gtttctctta 2600 tcaattggac tctcccaggt tccacagaac agtaatattt tttgaacaat 2650 aggtacaata gaaggtette tgteatttaa eetggtaaag geagggetgg 2700 agggggaaaa taaatcatta agcctttgag taacggcaga atatatggct 2750

gtagatccat ttttaatggt tcatttcctt tatggtcata taactgcaca 2800 gctgaagatg aaaggggaaa ataaatgaaa attttacttt tcgatgccaa 2850 tgatacattg cactaaactg atggaagaag ttatccaaag tactgtataa 2900 catcttgttt attatttaat gttttctaaa ataaaaaatg ttagtggttt 2950 tccaaatggc ctaataaaaa caattatttg taaataaaaa cactgttagt 3000 aat 3003

<210> 315

<211> 519

<212> PRT

<213> Homo Sapien

<400> 315

Met Asp Phe Leu Leu Ala Leu Val Leu Val Ser Ser Leu Tyr Leu
1 5 10 15

Gln Ala Ala Ala Glu Phe Asp Gly Arg Trp Pro Arg Gln Ile Val 20 25 30

Ser Ser Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys 35 40 45

Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Val Cys
50 55 60

Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys
65 70 75

Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu 80 85 90

Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met

95 100 105

Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met 110 115 120

Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met
125 130 135

Ala Asn Cys Gln Tyr Gly Cys Asp Val Val Lys Gly Gln Ile Arg 140 145 150

Cys Gln Cys Pro Ser Pro Gly Leu His Leu Ala Pro Asp Gly Arg 155 160 165

Thr	Сув	Val	Asp	Val 170	Asp	Glu	Cys	Ala	Thr 175	Gly	Arg	Ala	Ser	Cys 180
Pro	Arg	Phe	Arg	Gln 185	Cys	Val	Asn	Thr	Phe 190	Gly	Ser	Tyr	Ile	Cys 195
Lys	Cys	His	Lys	Gly 200	Phe	Asp	Leu	Met	Tyr 205	Ile	Gly	Gly	Lys	Tyr 210
Gln	Cys	His	Asp	Ile 215	Asp	Glu	Cys	Ser	Leu 220	Gly	Gln	Tyr	Gln	Cys 225
Ser	Ser	Phe	Ala	Arg 230	Cys	Tyr	Asn	Val	Arg 235	Gly	Ser	Tyr	Lys	Cys 240
Lys	Cys	Lys	Glu	Gly 245	Tyr	Gln	Gly	Asp	Gly 250	Leu	Thr	Cys	Val	Tyr 255
Ile	Pro	Lys	Val	Met 260	Ile	Glu	Pro	Ser	Gly 265	Pro	Ile	His	Val	Pro 270
Lys	Gly	Asn	Gly	Thr 275	Ile	Leu	Lys	Gly	Asp 280	Thr	Gly	Asn	Asn	Asn 285
Trp	Ile	Pro	Asp	Val 290	Gly	Ser	Thr	Trp	Trp 295	Pro	Pro	Lys	Thr	Pro 300
Tyr	Ile	Pro	Pro	Ile 305	Ile	Thr	Asn	Arg	Pro 310	Thr	Ser	Lys	Pro	Thr 315
Thr	Arg	Pro	Thr	Pro 320	Lys	Pro	Thr	Pro	Ile 325	Pro	Thr	Pro	Pro	Pro 330
Pro	Pro	Pro	Leu	Pro 335	Thr	Glu	Leu	Arg	Thr 340	Pro	Leu	Pro	Pro	Thr 345
Thr	Pro	Glu	Arg	Pro 350	Thr	Thr	Gly	Leu	Thr 355	Thr	Ile	Ala	Pro	Ala 360
Ala	Ser	Thr	Pro	Pro 365	Gly	Gly	Ile	Thr	Val 370	Asp	Asn	Arg	Val	Gln 375
Thr	Asp	Pro	Gln	Lys 380	Pro	Arg	Gly	Asp	Val 385	Phe	Ser	Val	Leu	Val 390
His	Ser	Cys	Asn	Phe 395	Asp	His	Gly	Leu	Cys 400	Gly	Trp	Ile	Arg	Glu 405
Lys	Asp	Asn	Asp		His	Trp	Glu	Pro		Arg	Asp	Pro	Ala	
				410					415					420
Gly	Gln	Tyr	Leu	Thr	Val	Ser	Ala	Ala	Lys	Ala	Pro	Gly	Gly	Lys

				425					430					435
Ala	Ala	Arg	Leu	Val 440	Leu	Pro	Leu	Gly	Arg 445	Leu	Met	His	Ser	Gly 450
Asp	Leu	Cys	Leu	Ser 455	Phe	Arg	His	Lys	Val 460	Thr	Gly.	Leu	His	Ser 465
Gly	Thr	Leu	Gln	Val 470	Phe	Val	Arg	Lys	His 475	Gly	Ala	His	Gly	Ala 480
Ala	Leu	Trp	Gly	Arg 485	Asn	Gly	Gly	His	Gly 490	Trp	Arg	Gln	Thr	Gln 495
Ile	Thr	Leu	Arg	Gly 500	Ala	Asp	Ile	Lys	Ser 505	Glu	Ser	Gln	Arg	
<210><211><211><212><213>	24 DN	A	cial	Seqi	uence	e								
<220> <223>		nthe	tic (Oligo	onuc:	leot:	ide 1	Probe	e					
<400> gatg			gctca	aagt	gc co	ctg :	24							
<210><211><212><213>	24 DN	A	cial	Seq	uence	е								
<220> <223>		nthe	tic (Olig	onuc:	leot	ide :	Prob	е					
<400> ttgc			agga	ccca	eg ta	acg :	24							
<210><211><211><212><213>	50 DN2	A	cial	Seq	uence	e								
<220> <223>		nthe	tic (Olig	onuc!	leot	ide :	Prob	e					
<400> ctga			gacc	tgtg	ta g	atgt	tgat	g aa	tgtg	ctac	agg	aaga	gcc !	50
<210><211><211>	21	10												

<213> Homo Sapien

<400> 319 cttctttgaa aaggattatc acctgatcag gttctctctg catttgcccc 50 tttagattgt gaaatgtggc tcaaggtctt cacaactttc ctttcctttg 100 caacaggtgc ttgctcgggg ctgaaggtga cagtgccatc acacactgtc 150 catggcgtca gaggtcaggc cctctaccta cccgtccact atggcttcca 200 cactccagca tcagacatcc agatcatatg gctatttgag agaccccaca 250 caatgcccaa atacttactg ggctctgtga ataagtctgt ggttcctgac 300 ttggaatacc aacacaagtt caccatgatg ccacccaatg catctctgct 350 tatcaaccca ctgcagttcc ctgatgaagg caattacatc gtgaaggtca 400 acattcaggg aaatggaact ctatctgcca gtcagaagat acaagtcacg 450 gttgatgatc ctgtcacaaa gccagtggtg cagattcatc ctccctctgg 500 ggctgtggag tatgtgggga acatgaccct gacatgccat gtggaagggg 550 gcactcggct agcttaccaa tggctaaaaa atgggagacc tgtccacacc 600 agetecacet acteettte tecceaaaac aataceette atattgetee 650 agtaaccaag gaagacattg ggaattacag ctgcctggtg aggaaccctg 700 tcagtgaaat ggaaagtgat atcattatgc ccatcatata ttatggacct 750 tatggacttc aagtgaattc tgataaaggg ctaaaagtag gggaagtgtt 800 tactgttgac cttggagagg ccatcctatt tgattgttct gctgattctc 850 atcccccaa cacctactcc tggattagga ggactgacaa tactacatat 900 atcattaagc atgggcctcg cttagaagtt gcatctgaga aagtagccca 950 gaagacaatg gactatgtgt gctgtgctta caacaacata accggcaggc 1000 aagatgaaac tcatttcaca gttatcatca cttccgtagg actggagaag 1050 cttgcacaga aaggaaaatc attgtcacct ttagcaagta taactggaat 1100 atcactattt ttgattatat ccatgtgtct tctcttccta tggaaaaaat 1150 atcaacccta caaagttata aaacagaaac tagaaggcag gccagaaaca 1200 gaatacagga aagctcaaac attttcaggc catgaagatg ctctggatga 1250 cttcqqaata tatqaatttq ttqcttttcc aqatgtttct ggtgtttcca 1300 qqattccaaq cagqtctgtt ccagcctctg attgtgtatc ggggcaagat 1350 ttqcacagta cagtgtatga agttattcag cacatccctg cccagcagca 1400 agaccatcca gagtgaactt tcatgggcta aacagtacat tcgagtgaaa 1450 ttctgaagaa acattttaag gaaaaacagt ggaaaagtat attaatctgg 1500 aatcagtgaa gaaaccagga ccaacacctc ttactcatta ttcctttaca 1550 tqcaqaataq aqqcatttat gcaaattgaa ctgcaggttt ttcagcatat 1600 acacaatgtc ttgtgcaaca gaaaaacatg ttggggaaat attcctcagt 1650 qqaqaqtcqt tctcatqctg acggggagaa cgaaagtgac aggggtttcc 1700 tcataagttt tgtatgaaat atctctacaa acctcaatta gttctactct 1750 acactttcac tatcatcaac actgagacta tcctgtctca cctacaaatg 1800 tggaaacttt acattgttcg atttttcagc agactttgtt ttattaaatt 1850 tttattagtg ttaagaatgc taaatttatg tttcaatttt atttccaaat 1900 ttctatcttg ttatttgtac aacaaagtaa taaggatggt tgtcacaaaa 1950 acaaaactat gccttctctt ttttttcaat caccagtagt atttttgaga 2000 agacttgtga acacttaagg aaatgactat taaagtctta tttttatttt 2050 tttcaaggaa agatggattc aaataaatta ttctgttttt gcttttaaaa 2100 aaaaaaaaa 2110

<210> 320

<211> 450

<212> PRT

<213> Homo Sapien

<400> 320

Met Trp Leu Lys Val Phe Thr Thr Phe Leu Ser Phe Ala Thr Gly
1 5 10 15

Ala Cys Ser Gly Leu Lys Val Thr Val Pro Ser His Thr Val His
20 25 30

Gly Val Arg Gly Gln Ala Leu Tyr Leu Pro Val His Tyr Gly Phe 35 40 45

His Thr Pro Ala Ser Asp Ile Gln Ile Ile Trp Leu Phe Glu Arg
50 55 60

Pro	His	Thr	Met	Pro 65	Lys	Tyr	Leu	Leu	Gly 70	Ser	Val	Asn	Lys	Ser 75
Val	Val	Pro	Asp	Leu 80	Glu	Tyr	Gln	His	Lys 85	Phe	Thr	Met	Met	Pro 90
Pro	Asn	Ala	Ser	Leu 95	Leu	Ile	Asn	Pro	Leu 100	Gln	Phe	Pro	Asp	Glu 105
Gly	Asn	Tyr	Ile	Val 110	Lys	Val	Asn	Ile	Gln 115	Gly	Asn	Gly	Thr	Leu 120
Ser	Ala	Ser	Gln	Lys 125	Ile	Gln	Val	Thr	Val 130	Asp	Asp	Pro	Val	Thr 135
Lys	Pro	Val	Val	Gln 140	Ile	His	Pro	Pro	Ser 145	Gly	Ala	Val	Glu	Tyr 150
Val	Gly	Asn	Met	Thr 155	Leu	Thr	Cys	His	Val 160	Glu	Gly	Gly		Arg 165
Leu	Ala	Tyr	Gln	Trp 170	Leu	Lys	Asn	Gly	Arg 175	Pro	Val	His	Thr	Ser 180
Ser	Thr	Tyr	Ser	Phe 185	Ser	Pro	Gln	Asn	Asn 190	Thr	Leu	His	Ile	Ala 195
Pro	Val	Thr	Lys	Glu 200	Asp	Ile	Gly	Asn	Tyr 205	Ser	Cys	Leu	Val	Arg 210
Asn	Pro	Val	Ser	Glu 215	Met	Glu	Ser	Asp	Ile 220	Ile	Met	Pro	Ile	Ile 225
Tyr	Tyr	Gly	Pro	Tyr 230	Gly	Leu	Gln	Val	Asn 235	Ser	Asp	Lys	Gly	Leu 240
Lys	Val	Gly	Glu	Val 245	Phe	Thr	Val	Asp	Leu 250	Gly	Glu	Ala	Ile	255
Phe	Asp	Cys	Ser	Ala 260	Asp	Ser	His	Pro	Pro 265	Asn	Thr	Tyr	Ser	Trp 3
Ile	Arg	Arg	Thr	Asp 275	Asn	Thr	Thr	Tyr	Ile 280	Ile	Lys	His	Gly	Pro 285
Arg	Leu	Glu	Val	Ala 290	Ser	Glu	Lys	Va1	Ala 295	Gln	Lys	Thr	Met	Asp 300
Tyr	Val	Cys	Cys	Ala 305	Tyr	Asn	Asn	Ile	Thr 310	Gly	Arg	Gln	Asp	Glu 315
Thr	His	Phe	Thr	Val	Ile	Ile	Thr	Ser	Val	Gly	Leu	Glu	Lys	Leu

				320					325					330
Ala	Gln	Lys	Gly	Lys 335	Ser	Leu	Ser	Pro	Leu 340	Ala	Ser	Ile	Thr	Gly 345
Ile	Ser	Leu	Phe	Leu 350	Ile	Ile	Ser	Met	Cys 355	Leu	Leu	Phe	Leu	Trp 360
Lys	Lys	Tyr	Gln	Pro 365	Tyr	Lys	Val	Ile	Lys 370	Gln	Lys	Leu	Glu	Gly 375
Arg	Pro	Glu	Thr	Glu 380	Tyr	Arg	Lys	Ala	Gln 385	Thr	Phe	Ser	Gly	His 390
Glu	Asp	Ala	Leu	Asp 395	Asp	Phe	Gly	Ile	Tyr 400	Glu	Phe	Val	Ala	Phe 405
Pro	Asp	Val	Ser	Gly 410	Val	Ser	Arg	Ile	Pro 415	Ser	Arg	Ser	Val	Pro 420
Ala	Ser	Asp	Cys	Val 425	Ser	Gly	Gln	Asp	Leu 430	His	Ser	Thr	Val	Tyr 435
Glu	Val	Ile	Gln	His 440	Ile	Pro	Ala	Gln	Gln 445	Gln	Asp	His	Pro	Glu 450
<210 × 211 × 212 × 213 ×	> 25 > DN	Ą	cial	Sequ	uence	e								
<220 <223		nthet	cic (Oligo	onuc:	leot:	ide 1	Probe	9					
<400; gato		l tca d	caaa	gcca	gt g	gtgc	25							
<210>	> 322	2												
<2113 <2123 <2133	> DNZ	_	cial	Seq	uence	e								
<220 <223		nthe	cic (Oligo	onuc:	leot	ide 1	Probe	e					
<400 cact		2 agg (gttc	ctca	ad da	agg :	24							
<210: <211: <212: <213:	> 45 > DN2	A	cial	Seq	uence	e								

<220>

<223> Synthetic Oligonucleotide Probe

<400> 323

ctccctctgg gctgtggagt atgtggggaa catgaccctg acatg 45

<210> 324

<211> 2397

<212> DNA

<213> Homo Sapien

<400> 324

gcaageggeg aaatggegee eteegggagt ettgeagtte eeetggeagt 50 cctgqtqctg ttgctttggg gtgctccctg gacgcacggg cggcggagca 100 acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150 tggatgatag aattttatgc cccgtggtgc cctgcttgtc aaaatcttca 200 accggaatgg gaaagttttg ctgaatgggg agaagatctt gaggttaata 250 ttgcgaaagt agatgtcaca gagcagccag gactgagtgg acggtttatc 300 ataactgctc ttcctactat ttatcattgt aaagatggtg aatttaggcg 350 ctatcagggt ccaaggacta agaaggactt cataaacttt ataagtgata 400 aagagtggaa gagtattgag cccgtttcat catggtttgg tccaggttct 450 gttctgatga gtagtatgtc agcactcttt cagctatcta tgtggatcag 500 gacgtgccat aactacttta ttgaagacct tggattgcca gtgtggggat 550 catatactgt ttttgcttta gcaactctgt tttccggact gttattagga 600 ctctgtatga tatttgtggc agattgcctt tgtccttcaa aaaggcgcag 650 accacageca tacccatace etteaaaaaa attattatea gaatetgeae 700 aacctttgaa aaaagtggag gaggaacaag aggcggatga agaagatgtt 750 tcagaagaag aagctgaaag taaagaagga acaaacaaag actttccaca 800 gaatgccata agacaacgct ctctgggtcc atcattggcc acagataaat 850 cctagttaaa ttttatagtt atcttaatat tatgattttg ataaaaacag 900 aagattgatc attttgtttg gtttgaagtg aactgtgact tttttgaata 950 ttgcagggtt cagtctagat tgtcattaaa ttgaagagtc tacattcaga 1000 acataaaagc actaggtata caagtttgaa atatgattta agcacagtat 1050 gatggtttaa atagttctct aatttttgaa aaatcgtgcc aagcaataag 1100 atttatgtat atttgtttaa taataaccta tttcaagtct gagttttgaa 1150 aatttacatt tcccaagtat tgcattattg aggtatttaa gaagattatt 1200 ttagagaaaa atatttctca tttgatataa tttttctctg tttcactgtg 1250 tgaaaaaaag aagatatttc ccataaatgg gaagtttgcc cattgtctca 1300 agaaatgtgt atttcagtga caatttcgtg gtctttttag aggtatattc 1350 caaaatttcc ttgtattttt aggttatgca actaataaaa actaccttac 1400 attaattaat tacagttttc tacacatggt aatacaggat atgctactga 1450 tttaqqaaqt ttttaagttc atggtattct cttgattcca acaaagtttg 1500 attttctctt gtatttttct tacttactat gggttacatt ttttattttt 1550 caaattggat gataatttct tggaaacatt ttttatgttt tagtaaacag 1600 tatttttttg ttgtttcaaa ctgaagttta ctgagagatc catcaaattg 1650 aacaatctgt tgtaatttaa aattttggcc acttttttca gattttacat 1700 cattettget gaactteaac ttgaaattgt tttttttte tttttggatg 1750 tgaaggtgaa cattcctgat ttttgtctga tgtgaaaaag ccttggtatt 1800 ttacattttg aaaattcaaa gaagcttaat ataaaagttt gcattctact 1850 caggaaaaag catcttcttg tatatgtctt aaatgtattt ttgtcctcat 1900 atacagaaag ttcttaattg attttacagt ctgtaatgct tgatgtttta 1950 aaataataac atttttatat tttttaaaag acaaacttca tattatcctg 2000 tgttctttcc tgactggtaa tattgtgtgg gatttcacag gtaaaagtca 2050 gtaggatgga acattttagt gtatttttac tccttaaaga gctagaatac 2100 atagttttca ccttaaaaga agggggaaaa tcataaatac aatgaatcaa 2150 ctgaccatta cgtagtagac aatttctgta atgtcccctt ctttctaggc 2200 tctgttgctg tgtgaatcca ttagatttac agtatcgtaa tatacaagtt 2250 ttctttaaag ccctctcctt tagaatttaa aatattgtac cattaaagag 2300 tttggatgtg taacttgtga tgccttagaa aaatatccta agcacaaaat 2350

aaacctttct aaccacttca ttaaagctga aaaaaaaaa aaaaaaa 2397

<210> 325

<211> 280

<212> PRT

<213> Homo Sapien

<400> 325

Met Ala Pro Ser Gly Ser Leu Ala Val Pro Leu Ala Val Leu Val 1 5 10 15

Leu Leu Trp Gly Ala Pro Trp Thr His Gly Arg Arg Ser Asn
20 25 30

Val Arg Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly
35 40 45

Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln 50 55 60

Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp
65 70 75

Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly 80 85 90

Leu Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile Tyr His
95 100 105

Cys Lys Asp Gly Glu Phe Arg Tyr Gln Gly Pro Arg Thr Lys 110 115 120

Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile 125 130 135

Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser

Ser Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys 155 160 165

His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro Val Trp Gly Ser 170 175 180

Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu 185 190 195

Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys 200 205 210

Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu

				215					220					225	
Ser	Glu	Ser	Ala	Gln 230	Pro	Leu	Lys	Lys	Val 235	Glu	Glu	Glu	Gln	Glu 240	
Ala	Asp	Glu	Glu	Asp 245	Val	Ser	Glu	Glu	Glu 250	Ala	Glu	Ser	Lys	Glu 255	
Gly	Thr	Asn	Lys	Asp 260	Phe	Pro	Gln	Asn	Ala 265	Ile	Arg	Gln	Arg	Ser 270	
Leu	Gly	Pro	Ser	Leu 275	Ala	Thr	Asp	Lys	Ser 280						
<211>	<210> 326 <211> 23 <212> DNA														
<213>	> Art	ific	cial	Sequ	ience	e									
<220> <223> Synthetic Oligonucleotide Probe															
<400> 326 tgaggtgggc aagcggcgaa atg 23															
<211:	<210> 327 <211> 20 <212> DNA <213> Artificial Sequence														
<220> <223> Synthetic Oligonucleotide Probe															
	<400> 327 tatgtggatc aggacgtgcc 20														
<211:	210> 328 2211> 21 2212> DNA 2213> Artificial Sequence														
<220 ×	220> 223> Synthetic Oligonucleotide Probe														
	400> 328 tgcagggttc agtctagatt g 21														
<210: <211: <212:															
-212	7~	-:-:	ai = 1	Com	ona	_									

```
<220>
<223> Synthetic Oligonucleotide Probe
<400> 329
ttgaaggaca aaggcaatct gccac 25
<210> 330
<211> 45
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 330
ggagtcttgc agttcccctg gcagtcctgg tgctgttgct ttggg 45
<210> 331
<211> 2168
<212> DNA
<213> Homo Sapien
<400> 331
 gcgagtgtcc agctgcggag acccgtgata attcgttaac taattcaaca 50
 aacgggaccc ttctgtgtgc cagaaaccgc aagcagttgc taacccagtg 100
 ggacaggcgg attggaagag cgggaaggtc ctggcccaga gcagtgtgac 150
 acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200
 ggtttggtgt cctgagctgt gtgcaggccg aattcttcac ctctattggg 250
 cacatgactg acctgattta tgcagagaaa gagctggtgc agtctctgaa 300
 agagtacatc cttgtggagg aagccaagct ttccaagatt aagagctggg 350
 ccaacaaaat qqaaqccttg actagcaagt cagctgctga tgctgagggc 400
 tacctggctc accctgtgaa tgcctacaaa ctggtgaagc ggctaaacac 450
 agactggcct gcgctggagg accttgtcct gcaggactca gctgcaggtt 500
 ttatcgccaa cctctctgtg cagcggcagt tcttccccac tgatgaggac 550
 gagataggag ctgccaaagc cctgatgaga cttcaggaca catacaggct 600
 ggacccaggc acaatttcca gaggggaact tccaggaacc aagtaccagg 650
 caatgctgag tgtggatgac tgctttggga tgggccgctc ggcctacaat 700
 gaaggggact attatcatac ggtgttgtgg atggagcagg tgctaaagca 750
```

gettgatgee ggggaggagg ceaceacaac caagteacag gtgetggaet 800 acctcagcta tgctgtcttc cagttgggtg atctgcaccg tgccctggag 850 ctcaccegec geetgetete cettgaceca ageeacgaac gagetggagg 900 gaatctgcgg tactttgagc agttattgga ggaagagaga gaaaaaacgt 950 taacaaatca gacagaagct gagctagcaa ccccagaagg catctatgag 1000 aggectgtgg actacetgee tgagagggat gtttacgaga geetetgteg 1050 tggggagggt gtcaaactga caccccgtag acagaagagg cttttctgta 1100 ggtaccacca tggcaacagg gccccacagc tgctcattgc ccccttcaaa 1150 gaggaggacg agtgggacag cccgcacatc gtcaggtact acgatgtcat 1200 gtctgatgag gaaatcgaga ggatcaagga gatcgcaaaa cctaaacttg 1250 cacgagccac cgttcgtgat cccaagacag gagtcctcac tgtcgccagc 1300 taccgggttt ccaaaagctc ctggctagag gaagatgatg accctgttgt 1350 ggcccgagta aatcgtcgga tgcagcatat cacagggtta acagtaaaga 1400 ctgcagaatt gttacaggtt gcaaattatg gagtgggagg acagtatgaa 1450 ccgcacttcg acttctctag gcgacctttt gacagcggcc tcaaaacaga 1500 ggggaatagg ttagcgacgt ttcttaacta catgagtgat gtagaagctg 1550 gtggtgccac cgtcttccct gatctggggg ctgcaatttg gcctaagaag 1600 ggtacagctg tgttctggta caacctcttg cggagcgggg aaggtgacta 1650 ccgaacaaga catgctgcct gccctgtgct tgtgggctgc aagtgggtct 1700 ccaataagtg gttccatgaa cgaggacagg agttcttgag accttgtgga 1750 tcaacagaag ttgactgaca teettttetg teetteeeet teetggteet 1800 tcagcccatg tcaacgtgac agacaccttt gtatgttcct ttgtatgttc 1850 ctatcagget gatttttgga gaaatgaatg tttgtctgga gcagagggag 1900 accatactag ggcgactcct gtgtgactga agtcccagcc cttccattca 1950 gcctgtgcca tccctggccc caaggctagg atcaaagtgg ctgcagcaga 2000 gttagctgtc tagcgcctag caaggtgcct ttgtacctca ggtgttttag 2050 gtgtgagatg tttcagtgaa ccaaagttct gataccttgt ttacatgttt 2100

gtttttatgg catttctatc tattgtggct ttaccaaaaa ataaaatgtc 2150 cctaccagaa aaaaaaaa 2168

<210> 332

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

Met Lys Leu Trp Val Ser Ala Leu Leu Met Ala Trp Phe Gly Val

Leu Ser Cys Val Gln Ala Glu Phe Phe Thr Ser Ile Gly His Met 20 25 30

Thr Asp Leu Ile Tyr Ala Glu Lys Glu Leu Val Gln Ser Leu Lys 35 40 45

Glu Tyr Ile Leu Val Glu Glu Ala Lys Leu Ser Lys Ile Lys Ser
50 55 60

Trp Ala Asn Lys Met Glu Ala Leu Thr Ser Lys Ser Ala Ala Asp
65 70 75

Ala Glu Gly Tyr Leu Ala His Pro Val Asn Ala Tyr Lys Leu Val 80 85 90

Lys Arg Leu Asn Thr Asp Trp Pro Ala Leu Glu Asp Leu Val Leu 95 100 105

Gln Asp Ser Ala Ala Gly Phe Ile Ala Asn Leu Ser Val Gln Arg 110 115 120

Gln Phe Phe Pro Thr Asp Glu Asp Glu Ile Gly Ala Ala Lys Ala 125 130 135

Leu Met Arg Leu Gln Asp Thr Tyr Arg Leu Asp Pro Gly Thr Ile 140 145 150

Ser Arg Gly Glu Leu Pro Gly Thr Lys Tyr Gln Ala Met Leu Ser 155 160 165

Val Asp Asp Cys Phe Gly Met Gly Arg Ser Ala Tyr Asn Glu Gly 170 175 180

Asp Tyr Tyr His Thr Val Leu Trp Met Glu Gln Val Leu Lys Gln 185 190 195

Leu Asp Ala Gly Glu Glu Ala Thr Thr Thr Lys Ser Gln Val Leu 200 205 210

Asp	Tyr	Leu	Ser	Tyr 215	Ala	Val	Phe	Gln	Leu 220	Gly	Asp	Leu	His	Arg 225
Ala	Leu	Glu	Leu	Thr 230	Arg	Arg	Leu	Leu	Ser 235	Leu	Asp	Pro	Ser	His 240
Glu	Arg	Ala	Gly	Gly 245	Asn	Leu	Arg	Tyr	Phe 250	Glu	Gln	Leu	Leu	Glu 255
Glu	Glu	Arg	Glu	Lys 260	Thr	Leu	Thr	Asn	Gln 265	Thr	Glu	Ala	Glu	Leu 270
Ala	Thr	Pro	Glu	Gly 275	Ile	Tyr	Glu	Arg	Pro 280	Val	Asp	Tyr	Leu	Pro 285
Glu	Arg	Asp	Val	Tyr 290	Glu	Ser	Leu	Cys	Arg 295	Gly	Glu	Gly	Val	Lys 300
Leu	Thr	Pro	Arg	Arg 305	Gln	Lys	Arg	Leu	Phe 310	Cys	Arg	Tyr	His	His 315
Gly	Asn	Arg	Ala	Pro 320	Gln	Leu	Leu	Ile	Ala 325	Pro	Phe	Lys	Glu	Glu 330
Asp	Glu	Trp	Asp	Ser 335	Pro	His	Ile	Val	Arg 340	Tyr	Tyr	Asp	Val	Met 345
Ser	Asp	Glu	Glu	Ile 350	Glu	Arg	Ile	Lys	Glu 355	Ile	Ala	Lys	Pro	Lys 360
Leu	Ala	Arg	Ala	Thr 365	Val	Arg	Asp	Pro	Lys 370	Thr	Gly	Val	Leu	Thr 375
Val	Ala	Ser	Tyr	Arg 380	Val	Ser	Lys	Ser	Ser 385	Trp	Leu	Glu	Glu	Asp 390
Asp	Asp	Pro	Val	Val 395	Ala	Arg	Val	Asn	Arg 400	Arg	Met	Gln	His	Ile 405
Thr	Gly	Leu	Thr	Val 410	Lys	Thr	Ala	Glu	Leu 415	Leu	Gln	Val	Ala	Asn 420
Tyr	Gly	Val	Gly	Gly 425	Gln	Tyr	Glu	Pro	His 430	Phe	Asp	Phe	Ser	Arg
Arg	Pro	Phe	Asp	Ser 440	Gly	Leu	Lys	Thr	Glu 445	Gly	Asn	Arg	Leu	Ala 450
Thr	Phe	Leu	Asn	Tyr 455	Met	Ser	Asp	Val	Glu 460	Ala	Gly	Gly	Ala	Thr 465
Val	Phe	Pro	Asp	Leu 470	Gly	Ala	Ala	Ile	Trp 475		Lys	Lys	Gly	Thr 480

```
Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr
                 485
                                      490
Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp
Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg
                                      520
                 515
Pro Cys Gly Ser Thr Glu Val Asp
                 530
<210> 333
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 333
ccaggcacaa tttccaga 18
<210> 334
<211> 19
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 334
 ggacccttct gtgtgccag 19
<210> 335
<211> 19
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 335
 ggtctcaaga actcctgtc 19
<210> 336
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
```

```
<400> 336
acactcagca ttgcctggta cttg 24
<210> 337
<211> 45
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 337
gggcacatga ctgacctgat ttatgcagag aaagagctgg tgcag 45
<210> 338
<211> 2789
<212> DNA
<213> Homo Sapien
<400> 338
gcagtattga gttttacttc ctcctctttt tagtggaaga cagaccataa 50
 tcccagtgtg agtgaaattg attgtttcat ttattaccgt tttggctggg 100
 ggttagttcc gacaccttca cagttgaaga gcaggcagaa ggagttgtga 150
 agacaggaca atettettgg ggatgetggt eetggaagee agegggeett 200
 gctctgtctt tggcctcatt gaccccaggt tctctggtta aaactgaaag 250
 cctactactg gcctggtgcc catcaatcca ttgatccttg aggctgtgcc 300
 cctggggcac ccacctggca gggcctacca ccatgcgact gagctccctg 350
 ttggctctgc tgcggccagc gcttcccctc atcttagggc tgtctctggg 400
 gtgcagcctg agcctcctgc gggtttcctg gatccagggg gagggagaag 450
 atccctgtgt cgaggctgta ggggagcgag gagggccaca gaatccagat 500
 tcgagagctc ggctagacca aagtgatgaa gacttcaaac cccggattgt 550
 cccctactac agggacccca acaagcccta caagaaggtg ctcaggactc 600
 ggtacatcca gacagagctg ggctcccgtg agcggttgct ggtggctgtc 650
 ctgacctccc gagctacact gtccactttg gccgtggctg tgaaccgtac 700
 ggtggcccat cacttccctc ggttactcta cttcactggg cagcgggggg 750
```

cccgggctcc agcagggatg caggtggtgt ctcatgggga tgagcggccc 800

gcctggctca tgtcagagac cctgcgccac cttcacacac actttggggc 850 cqactacgac tggttcttca tcatgcagga tgacacatat gtgcaggccc 900 cccgcctggc agcccttgct ggccacctca gcatcaacca agacctgtac 950 ttaggccggg cagaggagtt cattggcgca ggcgagcagg cccggtactg 1000 teatggggg tttggetace tgttgteacg gagteteetg ettegtetge 1050 ggccacatct ggatggctgc cgaggagaca ttctcagtgc ccgtcctgac 1100 gagtggcttg gacgctgcct cattgactct ctgggcgtcg gctgtgtctc 1150 acagcaccag gggcagcagt atcgctcatt tgaactggcc aaaaataggg 1200 accetgagaa ggaagggage teggetttee tgagtgeett egeegtgeae 1250 cctgtctccg aaggtaccct catgtaccgg ctccacaaac gcttcagcgc 1300 tctggagttg gagcgggctt acagtgaaat agaacaactg caggctcaga 1350 teeggaacet gacegtgetg acceeegaag gggaggeagg getgagetgg 1400 cccgttgggc tccctgctcc tttcacacca cactctcgct ttgaggtgct 1450 gggctgggac tacttcacag agcagcacac cttctcctgt gcagatgggg 1500 ctcccaagtg cccactacag ggggctagca gggcggacgt gggtgatgcg 1550 ttggagactg ccctggagca gctcaatcgg cgctatcagc cccgcctgcg 1600 cttccagaag cagcgactgc tcaacggcta tcggcgcttc gacccagcac 1650 ggggcatgga gtacaccctg gacctgctgt tggaatgtgt gacacagcgt 1700 gggcaccggc gggccctggc tcgcagggtc agcctgctgc ggccactgag 1750 ccgggtggaa atcctaccta tgccctatgt cactgaggcc acccgagtgc 1800 agetggtget gecaeteetg gtggetgaag etgetgeage eeeggettte 1850 ctcgaggcgt ttgcagccaa tgtcctggag ccacgagaac atgcattgct 1900 caccetgttg etggtetacg ggccacgaga aggtggeegt ggageteeag 1950 acccatttct tggggtgaag gctgcagcag cggagttaga gcgacggtac 2000 cctgggacga ggctggcctg gctcgctgtg cgagcagagg ccccttccca 2050 ggtgcgactc atggacgtgg tctcgaagaa gcaccctgtg gacactctct 2100

tettecttae caccgtgtgg acaaggeetg ggeeegaagt ceteaacege 2150
tgtegeatga atgecatete tggetggeag geettette cagtecattt 2200
ccaggagtte aateetgeee tgteaceae gagateaeee ecagggeece 2250
egggggetgg ecetgaeeee eceteceete etggtgetga eeeeteeegg 2300
ggggeteeta taggggggag atttgaeegg eaggettetg eggagggetg 2350
ettetaeaae getgaetaee tggeggeeeg ageeeggetg geaggtgaae 2400
tggeaggeea ggaagaggag gaageeetgg agggettga ggtgatggat 2450
gtttteetee ggtteteagg geteeaeete tttegggeeg tagageeagg 2500
getggtgeag aagtteteee tgegagaetg eageeeagge tagageeagg 2500
getggtgeag eagtteteee tgegagaetg eageeeagge eteagtgaag 2550
aaetetaeea eegetgeege eteageaaee tggagggee aggggeegt 2600
geeeagetgg etatggetet etttgageag gageaggeea atageaetta 2650
geeegeetgg gggeeetaae eteattaeet tteetttgte tgeeteagee 2700
eeaggaaggg eaaggeaaga tggtggaeag atagagaatt gttgetgtat 2750
tttttaaata tgaaaatgtt attaaaeatg tettetgee 2789

<400> 339

Met Arg Leu Ser Ser Leu Leu Ala Leu Leu Arg Pro Ala Leu Pro 1 5 10 15

Leu Ile Leu Gly Leu Ser Leu Gly Cys Ser Leu Ser Leu Leu Arg
20 25 30

Val Ser Trp Ile Gln Gly Glu Gly Glu Asp Pro Cys Val Glu Ala 35 40 45

Val Gly Glu Arg Gly Gly Pro Gln Asn Pro Asp Ser Arg Ala Arg
50 55 60

Leu Asp Gln Ser Asp Glu Asp Phe Lys Pro Arg Ile Val Pro Tyr
65 70 75

Tyr Arg Asp Pro Asn Lys Pro Tyr Lys Lys Val Leu Arg Thr Arg 80 85 90

Tyr Ile Gln Thr Glu Leu Gly Ser Arg Glu Arg Leu Leu Val Ala

<210> 339

<211> 772

<212> PRT

<213> Homo Sapien

•				95					100					105
Val	Leu	Thr	Ser	Arg 110	Ala	Thr	Leu	Ser	Thr 115	Leu	Ala	Val	Ala	Val 120
Asn	Arg	Thr	Val	Ala 125	His	His	Phe	Pro	Arg 130	Leu	Leu	Tyr	Phe	Thr 135
Gly	Gln	Arg	Gly	Ala 140	Arg	Ala	Pro	Ala	Gly 145	Met	Gln	Val	Val	Ser 150
His	Gly	Asp	Glu	Arg 155	Pro	Ala	Trp	Leu	Met 160	Ser	Glu	Thr	Leu	Arg 165
His	Leu	His ,	Thr	His 170	Phe	Gly	Ala	Asp	Tyr 175	Asp	Trp	Phe	Phe	Ile 180
Met	Gln	Asp	Asp	Thr 185	Tyr	Val	Gln	Ala	Pro 190	Arg	Leu	Ala	Ala	Leu 195
Ala	Gly	His	Leu	Ser 200	Ile	Asn	Gln	Asp	Leu 205	Tyr	Leu	Gly	Arg	Ala 210
Glu	Glu	Phe	Ile	Gly 215	Ala	Gly	Glu	Gln	Ala 220	Arg	Tyr	Cys	His	Gly 225
Gly	Phe	Gly	Tyr	Leu 230	Leu	Ser	Arg	Ser	Leu 235	Leu	Leu	Arg	Leu	Arg 240
Pro	His	Leu	Asp	Gly 245	Cys	Arg	Gly	Asp	Ile 250	Leu	Ser	Ala	Arg	Pro 255
Asp	Glu	Trp	Leu	Gly 260	Arg	Cys	Leu	Ile	Asp 265	Ser	Leu	Gly	Val	Gly 270
Cys	Val	Ser	Gln	His 275	Gln	Gly	Gln	Gln	Tyr 280	Arg	Ser	Phe	Glu	Leu 285
Ala	Lys	Asn	Arg	Asp 290	Pro	Glu	Lys	Glu	Gly 295	Ser	Ser	Ala	Phe	Leu 300
Ser	Ala	Phe	Ala	Val 305	His	Pro	Val	Ser	Glu 310	Gly	Thr	Leu	Met	Tyr 315
Arg	Leu	His	Lys	Arg 320	Phe	Ser	Ala	Leu	Glu 325	Leu	Glu	Arg	Ala	Tyr 330
Ser	Glu	Ile	Glu	Gln 335	Leu	Gln	Ala	Gln	Ile 340	Arg	Asn	Leu	Thr	Val 345
Leu	Thr	Pro	Glu	Gly 350	Glu	Ala	Gly	Leu	Ser 355	Trp	Pro	Val	Gly	Leu 360

Pro	Ala	Pro	Phe	Thr 365	Pro	His	Ser	Arg	Phe 370	Glu	Val	Leu	Gly	Trp 375
Asp	Tyr	Phe	Thr	Glu 380	Gln	His	Thr	Phe	Ser 385	Cys	Ala	Asp	Gly	Ala 390
Pro	Lys	Cys	Pro	Leu 395	Gln	Gly	Ala	Ser	Arg 400	Ala	Asp	Val	Gly	Asp 405
Ala	Leu	Glu	Thr	Ala 410	Leu	Glu	Gln	Leu	Asn 415	Arg	Arg	Tyr	Gln	Pro 420
Arg	Leu	Arg	Phe	Gln 425	Lys	Gln	Arg	Leu	Leu 430	Asn	Gly	Tyr	Arg	Arg 435
Phe	Asp	Pro	Ala	Arg 440	Gly	Met	Glu	Tyr	Thr 445	Leu	Asp	Leu	Leu	Leu 450
Glu	Cys	Val	Thr	Gln 455	Arg	Gly	His	Arg	Arg 460	Ala	Leu	Ala	Arg	Arg 465
Val	Ser	Leu	Leu	Arg 470	Pro	Leu	Ser	Arg	Val 475	Glu	Ile	Leu	Pro	Met 480
Pro	Tyr	Val	Thr	Glu 485	Ala	Thr	Arg	Val	Gln 490	Leu	Val	Leu	Pro	Leu 495
Leu	Val	Ala	Glu	Ala 500	Ala	Ala	Ala	Pro	Ala 505	Phe	Leu	Glu	Ala	Phe 510
Ala	Ala	Asn	Val	Leu 515	Glu	Pro	Arg	Glu	His 520	Ala	Leu	Leu	Thr	Leu 525
Leu	Leu	Val	Tyr	Gly 530	Pro	Arg	Glu	Gly	Gly 535	Arg	Gly	Ala	Pro	Asp 540
Pro	Phe	Leu	Gly	Val 545	Lys	Ala	Ala	Ala	Ala 550	Glu	Leu	Glu	Arg	Arg 555
Tyr	Pro	Gly	Thr	Arg 560	Leu	Ala	Trp	Leu	Ala 565	Val	Arg	Ala	Glu	Al a 570
Pro	Ser	Gln	Val	Arg 575	Leu	Met	Asp	Val	Val 580	Ser	Lys	Lys	His	Pro 585
Val	Asp	Thr	Leu	Phe 590	Phe	Leu	Thr	Thr	Val 595	Trp	Thr	Arg	Pro	Gly 600
Pro	Glu	Val	Leu	Asn 605	Arg	Суѕ	Arg	Met	Asn 610	Ala	Ile	Ser	Gly	Trp 615
Gln	Ala	Phe	Phe	Pro 620	Val	His	Phe	Gln	Glu 625	Phe	Asn	Pro	Ala	Leu 630

Ser	Pro	Gln	Arg	Ser 635	Pro	Pro	Gly	Pro	Pro 640	Gly	Ala	Gly	Pro	Asp 645
Pro	Pro	Ser	Pro	Pro 650	Gly	Ala	Asp	Pro	Ser 655	Arg	Gly	Ala	Pro	11e
Gly	Gly	Arg	Phe	Asp 665	Arg	Gln	Ala	Ser	Ala 670	Glu	Gly	Cys	Phe	Туг 675
Asn	Ala	Asp	Tyr	Leu 680	Ala	Ala	Arg	Ala	Arg 685	Leu	Ala	Gly	Glu	Let 690
Ala	Gly	Gln	Glu	Glu 695	Glu	Glu	Ala	Leu	Glu 700	Gly	Leu	Glu	Val	Met 705
Asp	Val	Phe	Leu	Arg 710	Phe	Ser	Gly	Leu	His 7 1 5	Leu	Phe	Arg	Ala	Val 720
Glu	Pro	Gly	Leu	Val 725	Gln	Lys	Phe	Ser	Leu 730	Arg	Asp	Cys	Ser	Pro 735
Arg	Leu	Ser	Glu	Glu 740	Leu	Tyr	His	Arg	Cys 745	Arg	Leu	Ser	Asn	Let 750
Glu	Gly	Leu	Gly	Gly 755	Arg	Ala	Gln	Leu	Ala 760	Met	Ala	Leu	Phe	Glu 765
Gln	Glu	Gln	Ala	Asn	Ser	Thr								

<210> 340

<211> 1572

<212> DNA

<213> Homo Sapien

<400> 340

cggagtggtg cgccaacgtg agaggaaacc cgtgcgcggc tgcgctttcc 50
tgtccccaag ccgttctaga cgcgggaaaa atgctttctg aaagcagctc 100
ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150
tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200
catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250
ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300
ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350
accaaacact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400

gtttgagtca attaatatgg acacaaatga catgtggtta atgatgagaa 450 aagcttacaa atacgccttt gataagtata gagaccaata caactggttc 500 ttccttgcac gccccactac gtttgctatc attgaaaacc taaagtattt 550 tttgttaaaa aaggatccat cacagccttt ctatctaggc cacactataa 600 aatctggaga ccttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650 gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagtg 700 tcctgaacag ggagggatga tttggaagat atctgaagat aaacagctag 750 cagtttgcct gaaatatgct ggagtatttg cagaaaatgc agaagatgct 800 gatggaaaag atgtatttaa taccaaatct gttgggcttt ctattaaaga 850 ggcaatgact tatcacccca accaggtagt agaaggctgt tgttcagata 900 tggctgttac ttttaatgga ctgactccaa atcagatgca tgtgatgatg 950 tatggggtat accgccttag ggcatttggg catattttca atgatgcatt 1000 ggttttctta cctccaaatg gttctgacaa tgactgagaa gtggtagaaa 1050 agcgtgaata tgatctttgt ataggacgtg tgttgtcatt atttgtagta 1100 gtaactacat atccaataca gctgtatgtt tctttttctt ttctaatttg 1150 gtggcactgg tataaccaca cattaaagtc agtagtacat ttttaaatga 1200 gggtggtttt tttctttaaa acacatgaac attgtaaatg tgttggaaag 1250 aagtgtttta agaataataa ttttgcaaat aaactattaa taaatattat 1300 atgtgataaa ttctaaatta tgaacattag aaatctgtgg ggcacatatt 1350 tttgctgatt ggttaaaaaa ttttaacagg tctttagcgt tctaagatat 1400 gcaaatgata tetetagttg tgaatttgtg attaaagtaa aaettttage 1450 tgtgtgttcc ctttacttct aatactgatt tatgttctaa gcctccccaa 1500 gttccaatgg atttgccttc tcaaaatgta caactaagca actaaagaaa 1550 attaaagtga aagttgaaaa at 1572

<210> 341

<211> 318

<212> PRT

<213> Homo Sapien

<400>														
Met 1	Leu	Ser	Glu	Ser 5	Ser	Ser	Phe	Leu	Lys 10	Gly	Val	Met	Leu	Gly 15
Ser	Ile	Phe	Cys	Ala 20	Leu	Ile	Thr	Met	Leu 25	Gly	His	Ile	Arg	Ile 30
Gly	His	Gly	Asn	Arg 35	Met	His	His	His	Glu 40	His	His	His	Leu	Gln 45
Ala	Pro	Asn	Lys	Glu 50	Asp	Ile	Leu	Lys	Ile 55	Ser	Glu	Asp	Glu	Arg 60
Met	Glu	Leu	Ser	Lys 65	Ser	Phe	Arg	Val	Tyr 70	Cys	Ile	Ile	Leu	Val 75
Lys	Pro	Lys	Asp	Val 80	Ser	Leu	Trp	Ala	Ala 85	Val	Lys	Glu	Thr	Trp 90
Thr	Lys	His	Cys	Asp 95	Lys	Ala	Glu	Phe	Phe 100	Ser	Ser	Glu	Asn	Val 105
Lys	Val	Phe	Glu	Ser 110	Ile	Asn	Met	Asp	Thr 115	Asn	Asp	Met	Trp	Leu 120
Met	Met	Arg	Lys	Ala 125	Tyr	Lys	Tyr	Ala	Phe 130	Asp	Lys	Tyr	Arg	Asp 135
Gln	Tyr	Asn	Trp	Phe 140	Phe	Leu	Ala	Arg	Pro 145	Thr	Thr	Phe	Ala	Ile 150
Ile	Glu	Asn	Leu	Lys 155	Tyr	Phe	Leu	Leu	Lys 160	Lys	Asp	Pro	Ser	Gln 165
Pro	Phe	Tyr	Leu	Gly 170	His	Thr	Ile	Lys	Ser 175	Gly	Asp	Leu	Glu	Туг 180
Val	Gly	Met	Glu	Gly 185	Gly	Ile	Val	Leu	Ser 190	Val	Glu	Ser	Met	Lys 195
Arg	Leu	Asn	Ser	Leu 200	Leu	Asn	Ile	Pro	Glu 205	Lys	Cys	Pro	Glu	Gln 210
Gly	Gly	Met	Ile	Trp 215	Lys	Ile	Ser	Glu	Asp 220	Lys	Gln	Leu	Ala	Val 225
Cys	Leu	Lys	Tyr	Ala 230	Gly	Val	Phe	Ala	Glu 235	Asn	Ala	Glu	Asp	Ala 240
Asp	Gly	Lys	Asp	Val 245	Phe	Asn	Thr	Lys	Ser 250	Val	Gly	Leu	Ser	Ile 255
Lys	Glu	Ala	Met	Thr	Tyr	His	Pro	Asn	Gln	Val	Val	Glu	Gly	Cys

270 260 265 Cys Ser Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln 275 280 Met His Val Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly His Ile Phe Asn Asp Ala Leu Val Phe Leu Pro Pro Asn Gly Ser 310 305 Asp Asn Asp <210> 342 <211> 23 <212> DNA <213> Artificial Sequence <220> <223> Synthetic Oligonucleotide Probe <400> 342 tccccaagcc gttctagacg cgg 23 <210> 343 <211> 18 <212> DNA <213> Artificial Sequence <220> <223> Synthetic Oligonucleotide Probe <400> 343 ctggttcttc cttgcacg 18 <210> 344 <211> 28 <212> DNA <213> Artificial Sequence <220> <223> Synthetic Oligonucleotide Probe <400> 344 gcccaaatgc cctaaggcgg tatacccc 28 <210> 345 <211> 50 <212> DNA <213> Artificial Sequence <220>

```
<223> Synthetic Oligonucleotide Probe
<400> 345
gggtgtgatg cttggaagca ttttctgtgc tttgatcact atgctaggac 50
<210> 346
<211> 25
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 346
gggatgcagg tggtgtctca tgggg 25
<210> 347
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 347
ccctcatgta ccggctcc 18
<210> 348
<211> 48
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 348
 ggattctaat acgactcact atagggctca gaaaagcgca acagagaa 48
<210> 349
<211> 47
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 349
 ctatgaaatt aaccctcact aaagggatgt cttccatgcc aaccttc 47
<210> 350
<211> 48
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Synthetic Oligonucleotide Probe
<400> 350
ggattctaat acgactcact atagggcggc gatgtccact ggggctac 48
<210> 351
<211> 48
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 351
ctatgaaatt aaccctcact aaagggacga ggaagatggg cggatggt 48
<210> 352
<211> 47
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 352
ggattctaat acgactcact atagggcacc cacgcgtccg gctgctt 47
<210> 353
<211> 48
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 353
ctatgaaatt aaccctcact aaagggacgg gggacaccac ggaccaga 48
<210> 354
<211> 48
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 354
ggattctaat acgactcact atagggcttg ctgcggtttt tgttcctg 48
<210> 355
<211> 48
```

```
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
ctatgaaatt aaccctcact aaagggagct gccgatccca ctggtatt 48
<210> 356
<211> 46
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
ggattctaat acgactcact atagggcgga tcctggccgg cctctg 46
<210> 357
<211> 48
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 357
ctatgaaatt aaccctcact aaagggagcc cgggcatggt ctcagtta 48
<210> 358
<211> 47
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 358
ggattctaat acgactcact atagggcggg aagatggcga ggaggag 47
<210> 359
<211> 48
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 359
 ctatgaaatt aaccctcact aaagggacca aggccacaaa cggaaatc 48
```

```
<210> 360
<211> 48
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
ggattctaat acgactcact atagggctgt gctttcattc tgccagta 48
<210> 361
<211> 48
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 361
ctatgaaatt aaccctcact aaagggaggg tacaattaag gggtggat 48
<210> 362
<211> 47
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
ggattctaat acgactcact atagggcccg cctcgctcct gctcctg 47
<210> 363
<211> 48
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 363
 ctatgaaatt aaccctcact aaagggagga ttgccgcgac cctcacag 48
<210> 364
<211> 47
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 364
```

```
ggattctaat acgactcact atagggcccc tcctgccttc cctgtcc 47
<210> 365
<211> 48
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 365
ctatgaaatt aaccctcact aaagggagtg gtggccgcga ttatctgc 48
<210> 366
<211> 48
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 366
ggattctaat acgactcact atagggcgca gcgatggcag cgatgagg 48
<210> 367
<211> 47
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 367
ctatgaaatt aaccctcact aaagggacag acggggcaga gggagtg 47
<210> 368
<211> 47
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 368
 ggattctaat acgactcact atagggccag gaggcgtgag gagaaac 47
<210> 369
<211> 48
<212> DNA
<213> Artificial Sequence
<220>
```

```
<223> Synthetic Oligonucleotide Probe
<400> 369
ctatgaaatt aaccctcact aaagggaaag acatgtcatc gggagtgg 48
<210> 370
<211> 48
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 370
ggattctaat acgactcact atagggccgg gtggaggtgg aacagaaa 48
<210> 371
<211> 48
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 371
ctatgaaatt aaccctcact aaagggacac agacagagcc ccatacgc 48
<210> 372
<211> 47
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 372
ggattctaat acgactcact atagggccag ggaaatccgg atgtctc 47
<210> 373
<211> 48
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 373
 ctatgaaatt aaccctcact aaagggagta aggggatgcc accgagta 48
<210> 374
<211> 47
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Synthetic Oligonucleotide Probe
<400> 374
ggattctaat acgactcact atagggccag ctacccgcag gaggagg 47
<210> 375
<211> 48
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 375
ctatgaaatt aaccctcact aaagggatcc caggtgatga ggtccaga 48
<210> 376
<211> 997
<212> DNA
<213> Homo Sapien
<400> 376
 cccacgcgtc cgatcttacc aacaaaacac tcctgaggag aaagaaagag 50
 aaaaaatgaa ttcatctaaa tcatctgaaa cacaatgcac agagagagga 150
 tgcttctctt cccaaatgtt cttatggact gttgctggga tccccatcct 200
 atttctcagt gcctgtttca tcaccagatg tgttgtgaca tttcgcatct 250
 ttcaaacctg tgatgagaaa aagtttcagc tacctgagaa tttcacagag 300
 ctctcctgct acaattatgg atcaggttca gtcaagaatt gttgtccatt 350
gaactgggaa tattttcaat ccagctgcta cttctttct actgacacca 400
 tttcctgggc gttaagttta aagaactgct cagccatggg ggctcacctg 450
 taaaatgaga gagtttttta ttggactgtc agaccaggtt gtcgagggtc 550
 agtggcaatg ggtggacggc acacctttga caaagtctct gagcttctgg 600
 gatgtagggg agcccaacaa catagctacc ctggaggact gtgccaccat 650
 gagagactct tcaaacccaa ggcaaaattg gaatgatgta acctgtttcc 700
 tcaattattt tcggatttgt gaaatggtag gaataaatcc tttgaacaaa 750
```

<210> 377

<211> 219

<212> PRT

<213> Homo Sapien

<400> 377

Met Asn Ser Ser Lys Ser Ser Glu Thr Gln Cys Thr Glu Arg Gly
1 5 10 15

Cys Phe Ser Ser Gln Met Phe Leu Trp Thr Val Ala Gly Ile Pro 20 25 30

Ile Leu Phe Leu Ser Ala Cys Phe Ile Thr Arg Cys Val Val Thr 35 40 45

Phe Arg Ile Phe Gln Thr Cys Asp Glu Lys Lys Phe Gln Leu Pro 50 55 60

Glu Asn Phe Thr Glu Leu Ser Cys Tyr Asn Tyr Gly Ser Gly Ser
65 70 75

Val Lys Asn Cys Cys Pro Leu Asn Trp Glu Tyr Phe Gln Ser Ser 80 85 90

Cys Tyr Phe Phe Ser Thr Asp Thr Ile Ser Trp Ala Leu Ser Leu 95 100 105

Lys Asn Cys Ser Ala Met Gly Ala His Leu Val Val Ile Asn Ser 110 115 120

Gln Glu Glu Gln Glu Phe Leu Ser Tyr Lys Lys Pro Lys Met Arg 125 130 135

Glu Phe Phe Ile Gly Leu Ser Asp Gln Val Val Glu Gly Gln Trp 140 145 150

Gln Trp Val Asp Gly Thr Pro Leu Thr Lys Ser Leu Ser Phe Trp
155 160 165

Asp Val Gly Glu Pro Asn Asn Ile Ala Thr Leu Glu Asp Cys Ala 170 175 180

```
Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val
                 185
                                      190
Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile
                 200
Asn Pro Leu Asn Lys Gly Lys Ser Leu
                 215
<210> 378
<211> 21
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 378
ttcagcttct gggatgtagg g 21
<210> 379
<211> 24
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 379
tattcctacc atttcacaaa tccg 24
<210> 380
<211> 49
<212> DNA
<213> Artificial Sequence
<223'> Synthetic oligonucleotide probe
<400> 380
ggaggactgt gccaccatga gagactcttc aaacccaagg caaaattgg 49
<210> 381
<211> 26
<212> DNA
<213> Artificial Sequence
<223> Synthetic oligonucleotide probe
<400> 381
gcagattttg aggacagcca cctcca 26
```

```
<210> 382
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
<400> 382
 ggccttgcag acaaccgt 18
<210> 383
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
<400> 383
 cagactgagg gagatccgag a 21
<210> 384
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
<400> 384
 cagetgeect teeceaacca 20
<210> 385
<211> 18
<212> DNA
<213> Artificial Sequence
<223> Synthetic oligonucleotide probe
<400> 385
 catcaagcgc ctctacca 18
<210> 386
<211> 21
<212> DNA
<213> Artificial Sequence
<223> Synthetic oligonucleotide probe
<400> 386
```

```
cacaaactcg aactgcttct g 21
<210> 387
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
<400> 387
 gggccatcac agctccct 18
<210> 388
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
<400> 388
gggatgtggt gaacacagaa ca 22
<210> 389
<211> 22
<212> DNA
<213> Artificial Sequence
<223> Synthetic oligonucleotide probe
<400> 389
 tgccagctgc atgctgccag tt 22
<210> 390
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
<400> 390
 cagaaggatg tcccgtggaa 20
<210> 391
<211> 17
<212> DNA
<213> Artificial Sequence
<220>
```

```
<223> Synthetic oligonucleotide probe
<400> 391
gccgctgtcc actgcag 17
<210> 392
<211> 21
<212> DNA
<213> Artificial Sequence
<223> Synthetic oligonucleotide probe
<400> 392
gacggcatcc tcagggccac a 21
<210> 393
<211> 20
<212> DNA
<213> Artificial Sequence
<223> Synthetic oligonucleotide probe
<400> 393
 atgtcctcca tgcccacgcg 20
<210> 394
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
<400> 394
 gagtgcgaca tcgagagctt 20
<210> 395
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
<400> 395
 ccgcagcctc agtgatga 18
<210> 396
<211> 21
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Synthetic oligonucleotide probe
<400> 396
gaagagcaca gctgcagatc c 21
<210> 397
<211> 22
<212> DNA
<213> Artificial Sequence
<223> Synthetic oligonucleotide probe
<400> 397
gaggtgtcct ggctttggta gt 22
<210> 398
<211> 20
<212> DNA
<213> Artificial Sequence
<223> Synthetic oligonucleotide probe
<400> 398
cctctggcgc ccccactcaa 20
<210> 399
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
<400> 399
 ccaggagagc tggcgatg 18
<210> 400
<211> 23
<212> DNA
<213> Artificial Sequence
<223> Synthetic oligonucleotide probe
<400> 400
gcaaattcag ggctcactag aga 23
<210> 401
<211> 29
```

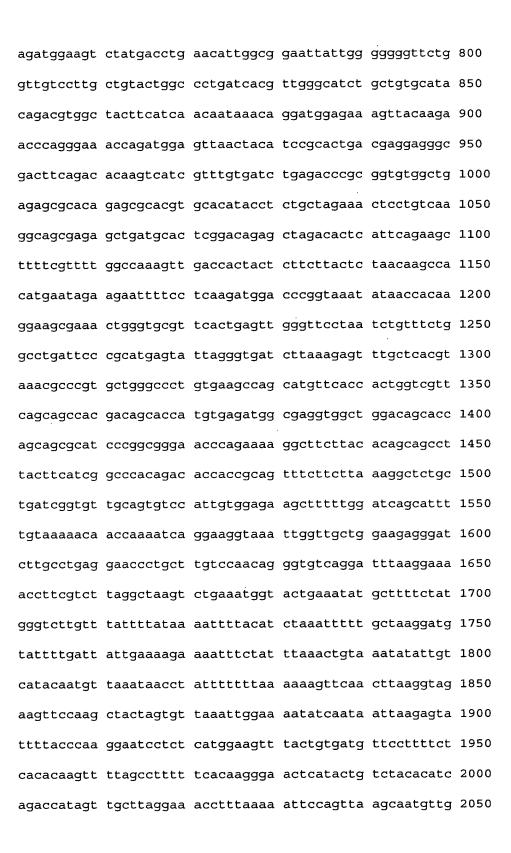
```
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
<400> 401
cacagagcat ttgtccatca gcagttcag 29
<210> 402
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
<400> 402
ggcagagact tccagtcact ga 22
<210> 403
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
<400> 403
gccaagggtg gtgttagata gg 22
<210> 404
<211> 24
<212> DNA
<213> Artificial Sequence
<223> Synthetic oligonucleotide probe
<400> 404
 caggecect tgatetgtac ccca 24
<210> 405
<211> 23
<212> DNA
<213> Artificial Sequence
<223> Synthetic oligonucleotide probe
<400> 405
 gggacgtgct tctacaagaa cag 23
```

```
<210> 406
<211> 26
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
<400> 406
caggettaca atgttatgat cagaca 26
<210> 407
<211> 31
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
tattcagagt tttccattgg cagtgccagt t 31
<210> 408
<211> 21
<212> DNA
<213> Artificial Sequence
<223> Synthetic oligonucleotide probe
<400> 408
tctacatcag cctctctgcg c 21
<210> 409
<211> 23
<212> DNA
<213> Artificial Sequence
<223> Synthetic oligonucleotide probe
<400> 409
 cgatcttctc cacccaggag cgg 23
<210> 410
<211> 18
<212> DNA
<213> Artificial Sequence
<223> Synthetic oligonucleotide probe
<400> 410
```

```
gccaggcctc acattcgt 18
<210> 411
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
<400> 411
 ctccctgaat ggcagcctga gca 23
<210> 412
<211> 24
<212> DNA
<213> Artificial Sequence
<223> Synthetic oligonucleotide probe
<400> 412
 aggtgtttat taagggccta cgct 24
<210> 413
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
<400> 413
 cagagcagag ggtgccttg 19
<210> 414
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
<400> 414
 tggcggagtc ccctcttggc t 21
<210> 415
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
```

```
<223> Synthetic oligonucleotide probe
<400> 415
ccctgtttcc ctatgcatca ct 22
<210> 416
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
<400> 416
 tcaaccctg accctttcct a 21
<210> 417
<211> 24
<212> DNA
<213> Artificial Sequence
<223> Synthetic oligonucleotide probe
<400> 417
 ggcagggac aagccatctc tcct 24
<210> 418
<211> 20
<212> DNA
<213> Artificial Sequence
<223> Synthetic oligonucleotide probe
<400> 418
 gggactgaac tgccagcttc 20
<210> 419
<211> 22
<212> DNA
<213> Artificial Sequence
<223> Synthetic oligonucleotide probe
<400> 419
 gggccctaac ctcattacct tt 22
<210> 420
<211> 23
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Synthetic oligonucleotide probe
<400> 420
tgtctgcctc agccccagga agg 23
<210> 421
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
<400> 421
tctgtccacc atcttgcctt g 21
<210> 422
<211> 3554
<212> DNA
<213> Homo Sapien
<400> 422
 gggactacaa gccgcgccgc gctgccgctg gcccctcagc aaccctcgac 50
 atggcgctga ggcggccacc gcgactccgg ctctgcgctc ggctgcctga 100
 cttcttcctg ctgctgcttt tcaggggctg cctgataggg gctgtaaatc 150
 tcaaatccag caatcgaacc ccagtggtac aggaatttga aagtgtggaa 200
 ctgtcttgca tcattacgga ttcgcagaca agtgacccca ggatcgagtg 250
 gaagaaaatt caagatgaac aaaccacata tgtgtttttt gacaacaaaa 300
 ttcagggaga cttggcgggt cgtgcagaaa tactggggaa gacatccctg 350
 aagatetgga atgtgacacg gagagaetca geeetttate getgtgaggt 400
 cgttgctcga aatgaccgca aggaaattga tgagattgtg atcgagttaa 450
 ctgtgcaagt gaagccagtg acccctgtct gtagagtgcc gaaggctgta 500
 ccagtaggca agatggcaac actgcactgc caggagagtg agggccaccc 550
 ccggcctcac tacagctggt atcgcaatga tgtaccactg cccacggatt 600
 ccagagccaa tcccagattt cgcaattctt ctttccactt aaactctgaa 650
 acaggcactt tggtgttcac tgctgttcac aaggacgact ctgggcagta 700
 ctactgcatt gcttccaatg acgcaggctc agccaggtgt gaggagcagg 750
```



aaatcagttt gcatctcttc aaaagaaacc tctcaggtta gctttgaact 2100 gcctcttcct gagatgacta ggacagtctg tacccagagg ccacccagaa 2150 gccctcagat gtacatacac agatgccagt cagctcctgg ggttgcgcca 2200 ggegeeeeg etetagetea etgttgeete getgtetgee aggaggeeet 2250 gccatccttg ggccctggca gtggctgtgt cccagtgagc tttactcacg 2300 tggcccttgc ttcatccagc acagctctca ggtgggcact gcagggacac 2350 tggtgtcttc catgtagcgt cccagctttg ggctcctgta acagacctct 2400 ttttggttat ggatggctca caaaataggg cccccaatgc tattttttt 2450 ttttaagttt gtttaattat ttgttaagat tgtctaaggc caaaggcaat 2500 tgcgaaatca agtctgtcaa gtacaataac atttttaaaa gaaaatggat 2550 cccactgttc ctctttgcca cagagaaagc acccagacgc cacaggctct 2600 gtcgcatttc aaaacaaacc atgatggagt ggcggccagt ccagcctttt 2650 aaagaacgtc aggtggagca gccaggtgaa aggcctggcg gggaggaaag 2700 tgaaacgcct gaatcaaaag cagttttcta attttgactt taaatttttc 2750 atccgccgga gacactgctc ccatttgtgg ggggacatta gcaacatcac 2800 tcagaageet gtgttettea agageaggtg tteteageet cacatgeeet 2850 gccgtgctgg actcaggact gaagtgctgt aaagcaagga gctgctgaga 2900 aggagcactc cactgtgtgc ctggagaatg gctctcacta ctcaccttgt 2950 ctttcagctt ccagtgtctt gggtttttta tactttgaca gctttttttt 3000 aattgcatac atgagactgt gttgactttt tttagttatg tgaaacactt 3050 tgccgcaggc cgcctggcag aggcaggaaa tgctccagca gtggctcagt 3100 gctccctggt gtctgctgca tggcatcctg gatgcttagc atgcaagttc 3150 cctccatcat tgccaccttg gtagagaggg atggctcccc accctcagcg 3200 ttggggattc acgctccagc ctccttcttg gttgtcatag tgatagggta 3250 gccttattgc cccctcttct tataccctaa aaccttctac actagtgcca 3300 tgggaaccag gtctgaaaaa gtagagagaa gtgaaagtag agtctgggaa 3350 gtagctgcct ataactgaga ctagacggaa aaggaatact cgtgtatttt 3400 aagatatgaa tgtgactcaa gactcgaggc cgatacgagg ctgtgattct 3450 gcctttggat ggatgttgct gtacacagat gctacagact tgtactaaca 3500 caccgtaatt tggcatttgt ttaacctcat ttataaaagc ttcaaaaaaa 3550 ccca 3554

<210> 423

<210> 423 <211> 310

<212> PRT

<213> Homo Sapien

<400> 423

Met Ala Leu Arg Arg Pro Pro Arg Leu Arg Leu Cys Ala Arg Leu 1 5 10 15

Pro Asp Phe Phe Leu Leu Leu Phe Arg Gly Cys Leu Ile Gly 20 25 30

Ala Val Asn Leu Lys Ser Ser Asn Arg Thr Pro Val Val Gln Glu 35 40 45

Phe Glu Ser Val Glu Leu Ser Cys Ile Ile Thr Asp Ser Gln Thr
50 55 60

Ser Asp Pro Arg Ile Glu Trp Lys Lys Ile Gln Asp Glu Gln Thr 65 70 75

Thr Tyr Val Phe Phe Asp Asn Lys Ile Gln Gly Asp Leu Ala Gly 80 85 90

Arg Ala Glu Ile Leu Gly Lys Thr Ser Leu Lys Ile Trp Asn Val 95 100 105

Thr Arg Arg Asp Ser Ala Leu Tyr Arg Cys Glu Val Val Ala Arg 110 115 120

Asn Asp Arg Lys Glu Ile Asp Glu Ile Val Ile Glu Leu Thr Val
125 130 135

Gln Val Lys Pro Val Thr Pro Val Cys Arg Val Pro Lys Ala Val 140 145 150

Pro Val Gly Lys Met Ala Thr Leu His Cys Gln Glu Ser Glu Gly
155 160 165

His Pro Arg Pro His Tyr Ser Trp Tyr Arg Asn Asp Val Pro Leu 170 175 180

Pro Thr Asp Ser Arg Ala Asn Pro Arg Phe Arg Asn Ser Ser Phe 185 190 195

His	Leu	Asn	Ser	Glu 200	Thr	Gly	Thr	Leu	Val 205	Phe	Thr	Ala	Val	His 210
Lys	Asp	Asp	Ser	Gly 215	Gln	Tyr	Tyr	Cys	Ile 220	Ala	Ser	Asn	Asp	Ala 225
Gly	Ser	Ala	Arg	Cys 230	Glu	Glu	Gln	Glu	Met 235	Glu	Val	Tyr	Asp	Leu 240
Asn	Ile	Gly	_	Ile 245	Ile	Gly	Gly	Val	Leu 250	Val	Val	Leu	Ala	Val 255
Leu	Ala	Leu	Ile	Thr 260	Leu	Gly	Ile	Cys	Cys 265	Ala	Tyr	Arg	Arg	Gly 270
Tyr	Phe	Ile	Asn	Asn	Lys	Gln	Asp	Gly	Glu	Ser	Tyr	Lys	Asn	Pro
				275					280					285
Gly	Lys	Pro	Asp	Gly 290	Val	Asn	Tyr	Ile	Arg 295	Thr	Asp	Glu	Glu	Gly 300
Asp	Phe	Arg	His	Lys 305	Ser	Ser	Phe	Val	Ile 310					